

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
		*						WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1733	Izug		173	205	0.0003	-0.16	0.17	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION
1733	2ero		173	205	0.0003	-0.59	0.29	CRO PROTEIN 2CRO 4	
1733	9ant	A	271	341	3.2e-26	-0.27	0.04	ANTENNAPEDIA PROTEIN; CHAIN: A; B; DNA; CHAIN: C, D; E; F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)
1734	1ahd	P	267	347	1.6e-28	-0.46	0.18	DNA-BINDING PROTEIN	
								ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 416 STRUCTURES) 1AHD 5	
1734	1b72	A	271	343	1.6e-24	-0.02	0.07	HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1734	1b8i	A	271	340	8e-24	-0.31	0.28	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEBOX PROTEIN	TRANSCRIPTION/DNA; ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,
								EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1734	1fj1	A	266	341	1.6e-23	-0.04	0.92	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF D score	SEQFOL D score	Compound	PDB annotation
1734 1fj	B	267	339	8e-22	0.38	1.00			PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1734 1fb		271	336	6e-24	0.61	0.99			TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR	
1734 1pra		173	205	0.00015	0.08	0.51			LFB 1 (HOMEODOMAIN) 1LFB 3	
1734 1r69		173	205	0.0003	0.15	0.78			GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA-BINDING 1PRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRUCTURES) 1PRA 4	
1734 1san		273	347	6.4e-26	0.09	0.19			GENE REGULATING PROTEIN REPRESSOR (AMINO-TERMINAL DOMAIN) (R1-69) 1R69 4	
1734 1zng									DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1734 2ero		173	205	0.0003	-0.16	0.17			PHAGE 434 CRO PROTEIN; CHAIN: NULL;	TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION
1734 9ant	A	271	341	8e-26	-0.27	0.04			CRO PROTEIN 2CRO 4	
									ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, PROTEIN(DNA) HD;	COMPLEX (DNA-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									D, E, F;	HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1738	1aj4	1	101	4.8e-30	-0.11	0.06			TROPONIN C; CHAIN: NULL;	muscle protein CTNC; cardiac muscle protein, regulatory, calcium binding
1738	1aj4	23	170	1.4e-38			82.97		TROPONIN C; CHAIN: NULL;	muscle protein CTNC; cardiac muscle protein, regulatory, calcium binding
1738	1aj4	25	169	1.4e-38	0.17	0.70			TROPONIN C; CHAIN: NULL;	muscle protein CTNC; cardiac muscle protein, regulatory, calcium binding
1738	1ak8	30	104	1.1e-29			75.36		CALMODULIN; CHAIN: NULL;	calcium-binding protein calmodulin cerium tric-domain, residues 1 - 75; cerium-loaded, calcium-binding protein
1738	1ap4	22	109	6.4e-23					CARDIAC N-TROPONIN C;	calcium-binding CTNC; calcium-binding, regulation, troponin C, cardiac muscle 2 contraction
1738	1au1	B	1	101	3.2e-20	0.08	-0.01		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	hydrolase calcineurin; hydrolase, phosphatase, immunosuppression
1738	1avs	A	26	106	3.2e-26			70.90	TROPONIN C; CHAIN: A, B;	muscle contraction, calmodulin-activated, tropinin, e-f hand 2 calcium-binding protein
1738	1blq		20	109	8e-27			71.63	N-TROPONIN C; CHAIN: NULL;	calcium-binding protein CTNC; calcium-binding, regulation, tropinin C, skeletal muscle
1738	1br1	B	33	170	4.8e-34			57.30	MYOSIN; CHAIN: A, B, C, D, E,	muscle protein MDE; muscle

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1738	1bu3		2	103	3.2e-11			50.72	F, G, H;	PROTEIN
1738	1cdm	A	1	102	8e-35	0.01	0.82		CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM BINDING CALCIUM BINDING
1738	1cdm	A	33	158	1.4e-47			85.63	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM_3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM_4	
1738	1cdm	A	33	169	1.4e-47	0.08	0.92		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM_3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM_4	
1738	1cll		1	102	3.2e-35	-0.09	0.40		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL_3	
1738	1cll		33	169	9.6e-53	-0.02	0.81		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL_3	
1738	1cll		33	170	9.6e-53			89.82	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL_3	
1738	1cmf		33	104	7.5e-23			68.52	CALMODULIN (VERTEBRATE); 1CMF_6 CHAIN: NULL; 1CMF_7 CALMODULIN APO TR2C-DOMAIN; 1CMF_9	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF_9
1738	1dtl	A	1	101	4.8e-29	0.00	0.28		CARDIAC TROPONIN C;	STRUCTURAL PROTEIN HELIX-

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1738	1dtl	A	31	169	9.6e-36	0.26	0.72		CHAIN: A; CARDIAC TROPONIN C; CHAIN: A;	TURN-HELIX STRUCTURAL PROTEIN HELIX- TURN-HELIX
1738	1exr	A	1	101	3.2e-34	-0.11	0.80		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1738	1exr	A	31	169	4.8e-51	0.03	0.89		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1738	1pva	A	7	104	1.6e-15			55.26	CALCIUM BINDING PARVALBUMIN (PIKE, P15.0, ALPHA COMPONENT) COMPLEXED WITH IPVAA 1 TWO CALCIUM IONS (SYNCHROTRON X-RAY DIFFRACTION) IPVAA 2	
1738	1rtp	1	7	104	3.2e-16			55.44	CALCIUM-BINDING PROTEIN ALPHA-PARVALBUMIN 1RTP 3	
1738	1tcf	1	101	1.1e-30	-0.10	0.35			TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1738	1tcf							89.65	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1738	1tcf		33	169	1.6e-41	-0.13	0.96		TROPONIN C; CHAIN: NULL,	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE

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1738	1tnx	1	101	9.6e-34	-0.26	0.41			TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1738	1tnx	24	169	1.6e-38			84.53		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1738	1tnx	33	169	1.6e-38	0.17	0.94			TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1738	1top	1	101	3.2e-32	-0.20	0.30			TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1738	1top	20	169	4.8e-42					CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1738	1top	33	169	4.8e-42	0.13	1.00			CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1738	1trc	A	36	103	8e-22				PROTEIN TROPONIN C 1TOP 3	
1738	1trf								CALCIUM BINDING PROTEIN CALMODULIN (TR=2-CS FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	
1738	1vfk	A	1	104	9.6e-36	-0.06	0.36		MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) ITRC 3	
1738	1vfk	A	31	170	1.1e-51				CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1738	1vfk	A	31	106	3.2e-26				CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2

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1738	1vk	A	33	169	1.1e-51	0.15	0.95		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1738	1wdc	B	33	170	7.5e-26			64.97	SCALLOP MYOSIN; CHAIN: A, B, C;	SCALLOP MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1738	1wdc	C	33	171	1.1e-25			54.16	SCALLOP MYOSIN; CHAIN: A, B, C;	SCALLOP MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1738	3ctn	31	104	8e-10				52.43	TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM BINDING PROTEIN
1738	4cpv	6	103	1.3e-11				51.70	CALCIUM BINDING CALCIUM- BINDING PARVALBUMIN (SP*I=4.25) 4CPV 3	
1745	1ukz	362	463	0.0006	-0.05	0.07			TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
1745	1zzak	A	362	587	0.0001	-0.17	0.13		ADENYLYLATE KINASE; CHAIN: A, B;	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3
1745	3adk								TRANSFERASE SEPHOSPHOTRANSFERASE ADENYLYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1746	1ukz	362	463	0.0006	-0.05	0.07			TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	

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1746 1zak	A	362	587	0.0001	-0.17	0.13		ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP:AMP-PHOSPHOTRANSFERASE, TRANSFERASE
1746 3adk		362	495	0.0075	-0.25	0.16		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1749 1btk	A	53	142	6e-06	-0.50	0.04		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK, TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
1749 1fao	A	55	142	3e-15	0.14	0.83		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1749 1fb8	A	48	142	3e-16	0.25	0.99		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1749 1fgy	A	52	142	7.5e-12	-0.02	0.75		GRP; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1750 1sm1	A	3	178	1.6e-14	0.08	-0.14		PENICILLINASE; CHAIN: A;	HYDROLASE METALLO-BETA-LACTAMASE, ANTIBIOTIC RESISTANCE, BINUCLEAR 2 ZINC, HYDROLASE

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1750	2bc2	A	3	170	1.6e-14	0.18	-0.05		METALLO BETA-LACTAMASE II; CHAIN: A, B;	HYDROLASE HYDROLASE, BETA-LACTAMASE, ANTIBIOTIC, METALLOENZYME
1751	1byt		1	711	0			253.58	LPOXYGENASE-3; CHAIN: NULL;	OXIDOREDUCTASE, OXIDOREDUCTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL
1751	1by4		35	711	0	0.36	1.00		LPOXYGENASE-3; CHAIN: NULL;	OXIDOREDUCTASE, OXIDOREDUCTASE, METALLOPROTEIN, FE(III) COMPLEX, CATECHOL
1751	1ca1		7	111	1.6e-20	-0.01	0.04		ALPHA-TOXIN; CHAIN: NULL;	HYDROLASE PHOSPHOLIPASE C, ZINC PHOSPHOLIPASE C, GANGRENE DETERMINANT, C2 DOMAIN, CA 2 AND MEMBRANE BINDING, HYDROLASE
1751	1eh	A	4	99	0.0045	0.46	0.45		TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLPASE; CHAIN: B, D	(HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE, COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION COMPLEX
1751	1lox		2	711	0	0.41	1.00		15-LPOXYGENASE; CHAIN: NULL;	OXIDOREDUCTASE 15LOX; OXIDOREDUCTASE, 15LO, DEPO1
1751	1lox		2	711	0			482.93	15-LPOXYGENASE; CHAIN: NULL;	OXIDOREDUCTASE 15LOX; OXIDOREDUCTASE, 15LO, DEPO2
1751	1yge		1	711	0			231.83	LPOXYGENASE-1; CHAIN: NULL;	DIOXYGENASE L-1; DIOXYGENASE, LPOXYGENASE, METALLOPROTEIN, FATTY ACIDS
1751	1yge		46	711	0	0.18	1.00		LPOXYGENASE-1; CHAIN: NULL;	DIOXYGENASE L-1; DIOXYGENASE, LPOXYGENASE, METALLOPROTEIN, FATTY ACIDS

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1753	1cc0	E	24	162	4.5e-66	0.50	1.00		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
1753	1cc0	E	24	177	9.6e-70	0.33	1.00		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
1753	1doa	B	5	162	6e-76	0.48	1.00		GTP-BINDING PROTEIN; CHAIN: A, GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY
1753	1doa	B	5	180	1.6e-78	0.48	1.00		GTP-BINDING PROTEIN; CHAIN: A, GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY
1757	1ahd	P	19	86	6.4e-36		70.63		DNA-BINDING PROTEIN ANTENNAPIEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1757	1ahd	P	20	85	6.4e-36	-0.12	0.90		DNA-BINDING PROTEIN ANTENNAPIEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1757	1b72	A	21	81	3e-31	-0.15	0.98		HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA

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1757	1b72	A	24	81	3.2e-28	0.19	0.99		HOMEobox PROTEIN HOX-B1; CHAIN: A; PBX; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1757	1b72	A	9	81	3e-31		64.24		HOMEobox PROTEIN HOX-B1; CHAIN: A; PBX; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1757	1b8i	A	20	77	6.4e-31		64.34		ULTRABITHORAX/HOMEBOTIC PROTEIN IV; CHAIN: A; HOMEobox PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOATIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1757	1b8i	A	2	78	6.4e-31	-0.14	0.82		ULTRABITHORAX/HOMEBOTIC PROTEIN IV; CHAIN: A; HOMEobox PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOATIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1757	1fz		18	86	4.8e-32			66.44	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1757	1fz		19	85	4.8e-32	-0.01	0.81		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1757	1oct	C	1	79	3e-31	-0.70	0.23		DNA-BINDING PROTEIN OCT-1 (POU DOMAIN) 1OCT 3	
1757	1san		25	86	1.6e-33			65.69	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) 1SAN 5	

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1757 1san		26	85	1.6e-33	-0.17	0.98		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1757 9ant	A	24	79	1.6e-33	-0.13	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)
1757 9ant	A	24	79	1.6e-33			68.97	ANTENNAPEDIA PROTEIN; CHAIN: A; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)
1758 1a3y	A	38	169	3e-35	0.63	0.86			LIPOCALIN LIPOCALIN, OLFACTION
1758 1dfv	A	20	169	4.5e-47	0.66	1.00		HUMAN NEUTROPHIL GELATINASE; CHAIN: A; B;	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL, NGAL, LIPOCALIN
1758 1ew3	A	30	169	1.4e-38	0.90	0.95		ALLERGEN EQU C 1; CHAIN: A;	ALLERGEN LIPOCALIN, BETA BARREL
1758 1mup		25	168	6e-37	0.78	1.00			PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 4
1758 1mup		25	168	6e-37			64.35	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE 1MUP 4	
1758 1obp	A	30	172	9e-36	0.19	-0.02		ODORANT-BINDING PROTEIN; CHAIN: A, B;	ODORANT-BINDING PROTEIN OBP OLFACTION, NOSE, TRANSPORT, LIPOCALIN, ODORANT-BINDING 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1758	1qgs	A	17	169	4.5e-40	0.83	1.00	NEUTROPHIL GELATINASE; CHAIN: A;	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL LIPOCALIN, SIGNAL PROTEIN, GLYCOPROTEIN
1758	1rbp		26	168	1e-35	0.14	-0.09	RETINOL TRANSPORT RETINOL BINDING PROTEIN 1RBP 3	PROTEIN
1758	2a2u	A	25	169	1.3e-36	0.69	0.99	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	GLOBULIN, LIPID BINDING PROTEIN
1758	2a2u	A	25	169	1.5e-37	0.91	1.00	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	LIPID BINDING PROTEIN A2U-GLOBULIN, LIPID BINDING PROTEIN
1758	2a2u	A	25	169	1.5e-37			ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	LIPID BINDING PROTEIN A2U-GLOBULIN, LIPID BINDING PROTEIN
1759	1afv	H	21	249	1.6e-94	0.30	1.00	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT, CHAIN: H, K, L, M;	CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24 COMPLEX (VIRAL PEPTIDE/RECEPTOR) HLA-A2-HEAVY CHAIN; CHAIN: B; T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
1759	1ao7	E	22	263	4.8e-64			HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2-HEAVY CHAIN; CHAIN: B; T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1aqk	H	22	252	1.6e-95	0.48	1.00	FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1759	1bd2	E	22	263	1.2e-98	0.74	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	PROPENSITY TO CRYSTALLIZE, ³ IMMUNOGLOBULIN COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1ba2	E	22	263	1.2e-98			386.70	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1dfb	H	21	232	9.6e-94	0.30	1.00		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
1759	1fvd	B	21	232	6.4e-96	0.41	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1759	1hpX	H	21	232	4.8e-95	0.47	1.00		IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROlytic, FAB, 2IMMUNOGLOBULIN
1759	1lgc	H	22	232	1.6e-95	0.21	1.00		COMPLEX (ANTIBODY BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1759	1igt	B	21	263	8e-99	0.42	0.99		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1759	Ingp	H	21	249	1.6e-93	0.35	1.00		NIG9 (IGG1-LAMBDA=); CHAIN: L, H;	REGION, IMMUNOGLOBULIN
1759	2iup	H	22	251	3.2e-93	0.39	1.00		MONOCLONAL ANTIBODY F11.2.32; CHAIN: L, H, M, N; HIV-1 PROTEASE PEPTIDE; CHAIN: P, Q;	IMMUNOGLOBULIN, IMMUNOGLOBULIN, COMPLEX (IMMUNOGLOBULIN/PEPTIDE) IMMUNOGLOBULIN, IGG1; FAB FRAGMENT, CR _{2.3} , REACTIVITY, HIV1 PROTEASE, ENZYME 2 INHIBITION, COMPLEX (IMMUNOGLOBULIN/PEPTIDE)
1762	1dan	L	64	195	6e-10			50.68	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C; AGGLUTININ ISOLECTIN VI; CHAIN: A	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1762	1ehd	A	12	88	1.1e-07	0.40	0.01			PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1762	1eis	A	12	88	3e-08	0.06	-0.12		AGGLUTININ ISOLECTIN VII/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1762	1en2	A	12	88	6e-09	-0.20	0.00		AGGLUTININ ISOLECTIN IAGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1762	1ext	A	37	192	3e-12			62.34	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1762	1ext	A	57	203	3e-12	-0.34	0.36		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1762	1fv1		31	101	1.2e-12	-0.37	0.04		FLAVORYDIN: IFV1-4 CHAIN:	BLOOD COAGULATION INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
					NULL IFVL 5					GP IIb/IIIa ANTAGONIST IFVL 9
1762	1klo		15	184	4.5e-19	0.17	-0.12		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1762	1klo		48	203	1.3e-20		66.44		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1762	Incf A	I7	140	7.5e-09	-0.24	0.23			TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
1762	Incf A	55	189	7.5e-11			55.28		TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
1762	1pfk	L	41	176	3e-14			57.36	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1762	1skz		19	121	3e-17	0.05	0.15		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR, FACTOR XA INHIBITOR, ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	1skz		57	161	1.5e-18			65.03	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR, FACTOR XA INHIBITOR, ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	1skz	58	161	3e-18	-0.14	0.12		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR, FACTOR XA INHIBITOR, ANTISTASIN CRYSTAL	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END T AA	Psi Blast score	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1762	1skz									STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1762	1vmo	A	35	190	9e-33	0.36	-0.15		ANTISTASIN; CHAIN: NULL; SERINE PROTEASE INHIBITOR, FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	
1762	2psp	A	90	191	0.0014			61.72	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	TREFOIL FAMILY OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL
1762	9wga	A	13	133	1.5e-18	0.12	0.13		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1762	9wga	A	32	191	6e-29			97.20	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1768	1bm		200	234	0.003	-0.02	0.70		BETA-SPECTRIN 1BTN 4	SIGNAL TRANSDUCTION PROTEIN
1768	1byn	A	245	347	0.0043	0.52	0.24		SYNAPTOTAGMIN 1; CHAIN: A; CHAIN: NULL; 1BTN 5	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS,
1768	1byn	A	245	349	1.2e-11	0.04	0.01		SYNAPTOTAGMIN 1; CHAIN: A;	NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS,
										NEUROTRANSMITTER 2 RELEASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1768	1dqy	A	247	362	4.5e-05	0.47	0.54		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
1768	1fao	A	173	235	6e-05	0.07	0.36		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1768	1fb8	A	173	239	9e-06	-0.29	0.70		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHSH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1768	1nf1	A	400	687	7.5e-68			108.36	NEUROFIBROMIN; CHAIN: A;	SIGNALING PROTEIN NF1-333; NEUROFIBROMIN, TYPE I NEUROFIBROMATOSIS, NF1, RAS, GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION, GTP 3 HYDROLYSIS, PATIENT MUTATION, ARGinine FINGER
1768	1nf1	A	416	682	7.5e-68	0.21	0.99		NEUROFIBROMIN; CHAIN: A;	SIGNALING PROTEIN NF1-333; NEUROFIBROMIN, TYPE I NEUROFIBROMATOSIS, NF1, RAS, GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION, GTP 3 HYDROLYSIS, PATIENT MUTATION, ARGinine FINGER
1768	1pls								PHOSPHORYLATION PLECKSTRIN (N-TERMINAL DOMAIN) MUTANT 1PLS_3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LHHHHH)) (NMR 25 STRUCTURES) 1PLS 5 SOS 1; CHAIN: NULL;	
1768 1pmx		162	235	0.00015	-0.48	0.39				SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1768 1qqg A		184	245	3e-05	0.17	0.16			INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A; B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION
1768 1rlw		247	349	6e-06	0.22	0.22			PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1768 1rsy		245	347	0.0043	-0.14	0.05			CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1768 1rsy		246	349	1.5e-09	0.13	0.49			CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1768 1wer		397	712	1.5e-91	0.62	1.00			P120GAP; CHAIN: NULL;	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER
1768 1wer		397	718	1.5e-91				183.05	P120GAP; CHAIN: NULL;	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER
1770 1b7f A		126	205	3.2e-14	0.05	-0.19			SXL-LETHAL PROTEIN; CHAIN: A; B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*)UP*	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1770	1cvj	B	352	435	1.6e-12	0.33	0.76		R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*3'); CHAIN: M, N, O, P, Q, R, S, T;	REGULATION/RNA
1770	1cvj	F	238	402	6.4e-21	0.17	0.65		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'. R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1770	1cvj	H	238	405	1.6e-21	0.03	0.25		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'. R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1770	1cvj	H	352	435	1.6e-12	0.78	0.68		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'. R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1770	1d8z	A	233	322	3.2e-21	0.04	0.19		HU ANTIGEN C; CHAIN: A; O, P, Q, R, S, T;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1770	1d8z	A	346	431	4.8e-13	0.52	0.27		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1770	1d9a	A	136	218	8e-14	0.03	-0.19		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1770	1d9a	A	237	319	3.2e-18	0.48	-0.03		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-

SEQ ID NO:	PDB ID	CHAI NID	STAR END TAA	Psi Blast AA	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1770	1fht		230	313	1.5e-11	0.57	0.12		BINDING DOMAIN RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPliceosome
1770	1fgc	A	222	313	3.2e-12	0.30	0.07	NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1770	1hal		129	314	4.8e-45	0.17	-0.09	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1770	1hal		231	425	1.6e-40	0.21	0.95	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1770	1hal		350	431	1.3e-16	0.83	0.94	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1770	1hd1	A	136	213	6.4e-20	0.03	-0.19	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	NUCLEAR PROTEIN RNA- BINDING DOMAIN
1770	1hd1	A	237	314	4.8e-22	0.78	0.16	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1770	1hd1	A	351	425	9.6e-15	0.91	0.68	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1770	1qm9	A	238	427	4.8e-19	0.06	0.15		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C19%, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP; RNA, SPlicing, 2 TRANSLATION
1770	1sxl		223	319	1.6e-18	0.21	-0.15		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN) 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1770	1sxl		341	429	3.2e-13	0.51	0.13		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN) 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1770	2mss	A	136	213	1.3e-14	0.11	-0.18		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	2mss	A	237	314	6.4e-19	0.74	0.17		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	2mss	A	351	425	4.8e-14	0.91	0.99		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1770	2sxl	*	236	322	1.1e-19	0.36	0.25		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPlicing
1770	2sxl		348	431	4.8e-14	0.42	0.70		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPlicing
1770	2u2f	A	236	314	6.4e-18	0.75	0.88		SPLICING FACTOR U2AF 65 KD	RNA-BINDING PROTEIN SPlicing, G,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1770	2up1	A	128	319	4.8e-47	0.00	0.09		SUBUNIT; CHAIN: A;	U2 SNRNP, RBD, RNA-BINDING PROTEIN COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1; U1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1770	2up1	A	231	433	1.6e-43	0.60	0.52		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	(RIBONUCLEOPROTEIN/DNA) HNRNP A1; U1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1770	3sx1	A	133	307	3.2e-36	0.22	-0.02		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1770	3sx1	A	236	425	1.4e-32	0.32	0.96		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1772	1alh	A	363	445	3.2e-31			74.27	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1772	1mey	C	138	219	9.6e-44	-0.22	0.04		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	166	247	4.8e-46	0.35	0.96		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	194	275	4.8e-47	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	222	303	1.3e-47	0.54	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	250	331	3.2e-48	0.24	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	278	359	1.1e-49	0.71	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	306	387	3.2e-50	0.74	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF D score	SEQFOL D score	Compound	PDB annotation
1772	1mey	C	334	415	1.6e-51	0.69	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	362	443	4.8e-51	-0.02	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	390	471	9.6e-51	0.37	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	418	499	1.6e-50	0.52	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	446	527	1.6e-50	0.31	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	446	528	1.6e-50	.	102.60		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	C	474	531	6.4e-34	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOIL D score	Compound	PDB annotation
1772	1mey	G	164	191	9.6e-11	0.55	0.05		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1mey	G	44	71	1.6e-09	-0.73	0.29		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	1tf6	A	167	312	1.3e-35	0.24	0.54		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1tf6	A	223	368	4.8e-37	0.28	0.96		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1tf6	A	307	452	3.2e-38	0.07	0.99		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1772	1tf6	A	334	497	3.2e-38			100.49	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	PsiBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN)
1772	1tfs	A	363	509	1.6e-37	-0.06	0.95		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION(DNA)) COMPLEX (TRANSCRIPTION REGULATION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN)
1772	1tfs	A	391	529	1.4e-36	0.01	0.94		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION(DNA)) COMPLEX (TRANSCRIPTION REGULATION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN)
1772	1ubd	C	143	247	4.8e-32	0.07	0.11		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA)) YNG-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION REGULATION(DNA)
1772	1ubd	C	169	275	1.5e-23	-0.21	0.72		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA)) YNG-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF D score	SEQPOL D score	Compound	PDB annotation
1772	1ubd	C	199	303	4.5e-43	0.13	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) COMPLEX (TRANSCRIPTION REGULATION(DNA)) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	1ubd	C	202	303	1.6e-32	0.02	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) COMPLEX (TRANSCRIPTION REGULATION(DNA)) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	1ubd	C	223	359	1.5e-46	0.21	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) COMPLEX (TRANSCRIPTION REGULATION(DNA)) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	1ubd	C	258	359	4.8e-34	0.36	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) COMPLEX (TRANSCRIPTION REGULATION(DNA)) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	1ubd	C	332	443	1.5e-50	0.03	1.00	YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	Iubd	C	360	472	6e-52	0.06	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	Iubd	C	388	499	9e-51	-0.01	0.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	Iubd	C	416	527	3e-50	0.01	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)
1772	Iubd	C	420	528	9e-51			82.44	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION) REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NC:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
								CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION (TRANSCRIPTION/DNA)
1772	lubb	C	426	527	8e-35	0.11	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION (TRANSCRIPTION/DNA)
1772	2adr		139	193	8e-14	0.11	-0.18	ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1772	2gli	A	102	246	3.2e-29	-0.10	0.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	197	389	3e-58	0.26	0.95	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	278	417	9e-64	0.51	1.00	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	306	445	1.5e-63	0.21	0.99	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	362	501	1.5e-67	0.31	0.98	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ D NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1772	2gii	A	362	501	1.5e-67			ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	390	524	1.5e-49	-0.07	0.84	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	398	529	1.6e-34	0.24	1.00	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1774	1bor		10	59	4.8e-06	-0.87	0.07	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2; TRANSCRIPTION REGULATION
1774	1chc		11	59	1.3e-11	-0.50	0.52	VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1774	1chc		15	63	3.2e-06	-0.28	0.39	VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1774	1fbv	A	14	69	1.2e-12	0.41	0.41	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1774	1fbv	A	15	59	3.2e-06	-0.34	0.21	SIGNAL TRANSDUCTION	LIGASE CBL, UBCH7, ZAP-70, E2,

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1774	1ffe		93	128	1.5e-13	-0.23	0.36		NUCLEAR FACTOR XNFK7; CHAIN: NULL;	ZINC-BINDING PROTEIN ZINC-BINDING PROTEIN XNFK7, BBOX, DEVELOPMENT, 3 MID-BLASTULA-TRANSITION
	1g25	A	11	70	4.5e-14	0.21	0.74		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
1774	1quu	A	63	304	3e-06		54.69		HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-Helix COILED COIL, CONTRACTILE PROTEIN
1774	1rnd		11	100	4.5e-20	-0.03	0.84		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN Y(D) RECOMBINATION ACTIVATING PROTEIN 1; RAG1, Y(D) RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1774	1rnd		9	109	6.4e-14	-0.19	0.01		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN Y(D) RECOMBINATION ACTIVATING PROTEIN 1; RAG1, Y(D) RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1775	1cun	A	248	414	4.5e-07	-0.07	0.19		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 1 AND 23 3-HELIX COILED-COILS,

SEQ ID NO:	PDB ID	CMAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMIF score	SEQPOL D score	Compound	PDB annotation
1776	1cun	A	1	93	9e-10	0.34	-0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1776	1ez3	A	9	124	4.5e-09	0.10	-0.12		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDa PROTEIN, P35A, THREE HELIX BUNDLE
1777	1chc			516	553	0.0006	0.21	0.18	VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) ICHC 3 (NMR, 1 STRUCTURE) ICHC 4	
1780	1eo0	A	1	78	4.5e-06	-0.14	0.52		TRANSCRIPTION ELONGATION FACTOR SII; CHAIN: A;	TRANSCRIPTION HELIX-BUNDLE
1780	1qyp		291	343	0.00045	-0.51	0.51		RNA POLYMERASE II; CHAIN: NULL;	TRANSCRIPTION TRANSCRIPTION, RNA POLYMERASE II SUBUNIT, RPB9, ZN RIBBON, 2 HYPERTHERMOPHILIC, EXTREMOPHILE
1780	1tfi			286	345	1.6e-10	0.16	1.00	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIIS, NUCLEARIC-ACID 1TFI3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI4	
1780	1tfi		287	343	4.5e-11	-0.07	0.75		TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF D score	SEQFOL D score	Compound	PDB annotation
									(TFIIS, NUCLEARIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	
1781	1aoj	A	438	510	1.5e-14	-0.85	0.01		EPS8; CHAIN: A, B;	SIGNAL TRANSDUCTION SRC HOMOLOGY DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, EPS8, PROLINE RICH PEPTIDE
1781	1awj		436	507	3e-14	0.30	0.82		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1781	1awo		459	508	1.2e-11	-0.29	0.92		ABL TYROSINE KINASE; CHAIN: NULL;	KINASE KINASE, SH3 DOMAIN, TRANSFERASE, PHOSPHOTRANSFERASE, 2 PROTO-ONCOGENE, MULTIPLE DOMAIN, LEUKEMIA
1781	1bbz	A	459	508	1e-11	-0.27	0.84		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41; CHAIN: B, D, F, H;	COMPLEX (TRANSFERASE/PEPTIDE)
1781	1bu1	A	459	508	4.5e-12	-0.27	1.00		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	COMPLEX (TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1781	1ddm	A	48	148	0.003	-0.04	0.63		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
1781	1efh	A	459	507	6e-11	-0.15	1.00		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SR E LOGY 3

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
									PROTEIN; CHAIN: B, D;	DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPI HELIX, PXXP MOTIF TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1781	1fyn	A	457	508	1e-11	0.07	1.00		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	
1781	1gbq	A	454	508	1.4e-12	-0.33	0.84		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1781	1gbr	A	446	510	3e-13	-0.35	0.74			COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
1781	1lck	A	456	581	4.8e-19	-0.41	0.01		P56=LCK= TYROSINE KINASE; 1LCK 7 CHAIN: A; 1LCK 8 TAIL PHOSPHOPEPTIDE TEGQPHOSPHOYQQPA;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1781	1ln0	C	459	507	3e-11	0.18	1.00		ILCK 14 CHAIN; B; ILCK 15 C-SRC; CHAIN; C; NLI (MN7-MN2-MN1-PLPPLP); CHAIN; N;	COMPLEX DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1781	1pwt		457	508	3e-10	0.21	1.00		ALPHA SPECTRIN; CHAIN; NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1781	1qcf	A	456	581	3.2e-18	-0.31	0.15		HAEMATOPOETIC CELL KINASE (HCK); CHAIN; A;	TYROSINE KINASE, PROTEIN KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1781	1qkw	A	457	508	1.5e-10	0.20	1.00		ALPPA II SPECTRIN; CHAIN; A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
1781	1qly	A	455	508	3e-12	-0.05	0.81		TYROSINE-PROTEIN KINASE BTK; CHAIN; A;	TYROSINE-PROTEIN KINASE, Brutons TYROSINE KINASE, CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1781	1shf	A	459	508	7.5e-11	-0.64	1.00		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1781	2nmb	A	27	153	3e-12	0.25	0.64		NUMB PROTEIN; CHAIN; A; GPPY PEPTIDE; CHAIN; B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETRIC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION
1781	4hck		455	508	7.5e-12	0.46	1.00		HEMATOPOETIC CELL	TRANSFERASE HCK; SH3, PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
								KINASE; CHAIN: NULL;	TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1782	1bg1	A	36	198	1.1e-07	0.07	0.04	STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	
1782	1bz4	A	9	126	1.6e-05	0.20	0.04	APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3; LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
1782	1cun	A	24	259	3e-13	0.04	-0.06	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1782	1dn1	B	78	298	7.5e-19	-0.22	0.30	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1782	1ez3	A	118	260	4.5e-07	0.11	0.28	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOAGM1 ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1782	1ez3	A	138	298	1.5e-08	-0.41	0.00	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOAGM1 ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1782	1ez3	A	246	394	1e-09	-0.04	0.18	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOAGM1 ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOIL D score	Compound	PDB annotation
1782	1fio	A	283	485	7.5e-07	-0.09	0.04	SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1782	1fio	A	59	280	1e-11	-0.28	0.03	SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1783	1aab		716	763	0.00012	-0.24	0.03	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN; NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMGB-BOX 1AAB 20
1783	1dg3	A	2237	2333	4.5e-05	0.02	0.19	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1783	1f5n	A	2237	2333	0.00015	0.02	0.04	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPNNP, GPPNHP.
1783	1faq		69	99	0.003	-0.40	0.03	RAF-1; CHAIN: NULL;	SERINE/THREONINE PROTEIN KINASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, 2 PROTO-ONCOGENE, ZINC, ATP-BINDING, PHORBOL-ESTER BINDING
1783	1hme		716	753	0.0045	-0.29	0.00	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING IHME 3 HMGB-BOX DOMAIN B OF RAT HMG1) (NMR, 1 STRUCTURE) IHME 4	
1783	1ncf	A	17	141	0.006	0.02	0.12	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN; A,	SIGNALING PROTEIN TYPE 1 RECEPTOR, STNFR1; INCF 8

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMUT score	SEQFOL D score	Compound	PDB annotation
1783	Iptq		21	50	0.003	0.02	0.23		B;INCF 5	BINDING PROTEIN, CYTOKINE INCF 19
1783	1tbn		21	50	0.00075	-0.09	0.31		PROTEIN KINASE C DELTA TYPE; IPTQ 4	PHOSPHOTRANSFERASE
1783	1tbn		69	99	0.006	-0.35	0.41		PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE
1783	2lef	A	716	763	7.5e-05	-0.13	0.31		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BINDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1784	1tbn		100	137	0.0009	-0.65	0.01		PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE
1785	1ahl	A	62	130	3.2e-26	-0.30	0.45		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B; C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1785	1bb0		178	232	3.2e-12	0.07	-0.13		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111 BBO ₃ REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) IBB0	

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1785	1bb0		64	113	1.6e-12	-0.88	0.04		4	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP1 MUTANT WITH CYS 111 BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) BBO 4
1785	1mey	C	15	86	1.6e-42	-0.42	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1785	1mey	C	43	114	4.8e-41	-0.19	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1785	1mey	G	87	114	3.2e-12	-0.23	0.05		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1785	2adr		62	117	4.8e-18	-0.01	0.90		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1788	1awc	B	18	157	8e-34	-0.23	0.52		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1788	lawc	B	3	125	4.8e-29	-0.09	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,
1788	1bd8		21	160	8e-27	-0.01	0.19		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TRANSCRIPTION 3 FACTOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1788	1bi7	B	443	560	6.4e-17	0.14	0.04		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	ONCOGENE CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1788	1blk	B	21	160	6.4e-26	-0.17	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1788	1blk	B	50	183	1.3e-23	0.01	0.37		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1788	1bu9	A	1	130	6.4e-25	-0.12	0.15		CYCLIN-DEPENDENT KINASE	HORMONE/GROWTH FACTOR P18-

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1788	1d9s	A	443	567	1.6e-17	0.14	0.06	6 INHIBITOR; CHAIN: A;	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1788	1ihb	A	18	161	1.3e-25	-0.12	0.10	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1788	1ihb							CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1788	1ihb	A	1	129	3.2e-24	0.01	0.37	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1788	1myo							MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1791	1bt0	A	124	194	1.4e-20	0.17	0.92	UBIQUITIN-LIKE PROTEIN 7, RUB; CHAIN: A;	SIGNALING PROTEIN RUB1, UBIQUITIN-LIKE PROTEIN, ARABIDOPSIS, SIGNALING PROTEIN
1791	1c3t	A	124	196	1.6e-27	0.02	0.76	1D8 UBIQUITIN; CHAIN: A;	DE NOVO PROTEIN PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC, 2 UBIQUITIN, DE NOVO PROTEIN, UBIQUITIN
1791	1ndd	A	124	195	6.4e-20	0.22	0.75	UBIQUITIN-LIKE PROTEIN NEDD8; CHAIN: A, B, C, D;	SIGNALING PROTEIN NEDD8; NEDD8, NEDD-8, UBIQUITIN-LIKE, PROTEOLYSIS, SIGNALING 2 PROTEIN
1791	1tbe	B	124	193	3.2e-27	0.48	0.94	UBIQUITIN TETRAUBIQUITIN LIBE 3	

SEQ NO.	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1791	1ubi	124	196	4.8e-29	0.19	0.66			CHROMOSOMAL PROTEIN UBIQUITIN 1UBI_3	
1791	1ud7	A	124	196	3.2e-28	0.39	0.55		UBIQUITIN CORE MUTANT ID7; CHAIN: A;	UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT
1791	1vcb	A	124	181	6.4e-05	-0.54	0.15		ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION
1792	1bax	1	92	3.2e-36	-0.22	0.64			M-PMV MATRIX PROTEIN; CHAIN: NULL;	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPYROTEIN, MYRISTYLATION
1792	1bax	1	92	3.2e-36			69.49		M-PMV MATRIX PROTEIN; CHAIN: NULL;	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPYROTEIN, MYRISTYLATION
1794	1dn1	B	157	227	0.0075	-0.04	0.00		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1795	1dn1	B	165	235	0.0075	-0.04	0.00		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1799	1aj4		225	382	6.4e-36			57.92	TROPONIN C; CHAIN: NULL;	muscle protein CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1799	1aj4		241	379	6.4e-36	0.30	0.25		TROPONIN C; CHAIN: NULL;	muscle protein CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1799	1ak8		241	309	4.8e-16	0.12	-0.01		CALMODULIN; CHAIN: NULL;	CALMODULIN-BINDING PROTEIN CALMODULIN CERJUM TRIC- DOMAIN, RESIDUES 1 - 75; CERJUM-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1799	1ap4			241	314	1.4e-12	0.50	-0.01	CARDIAC N-TROPONIN C; CHAIN: NULL;	LOADED CALCIUM-BINDING PROTEIN
1799	1au1	B		233	391	4.8e-42			SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTION
1799	1au1	B		240	378	4.8e-42	0.46	0.68	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1799	1bjf	A		202	345	3.2e-11	-0.02	0.19	NEUROCALCIN DELTA; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1799	1bjf	A		224	385	6.4e-36	0.64	0.83	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1799	1bjf	A		224	390	6.4e-36			NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1799	1cdm	A		241	378	3.2e-42	0.25	0.18	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4 1CLL 3	CALCIUM-BINDING CALMODULIN (VERTEBRATE)
1799	1cll			241	378	3.2e-47	0.05	0.21		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)
1799	1cll			241	380	3.2e-47			59.19	CALCIUM-BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1799	1cmf								CALMODULIN (VERTEBRATE); ICLL 3	
1799	1cmf	242	309	4.8e-11	0.73	0.13			CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN; NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1799	1cmf	310	378	1.6e-25	0.43	-0.06			CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN; NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1799	1dgv	A	241	388	3.2e-20	0.01	0.60		APO C1B; CHAIN: A;	BLOOD CLOTHING HELICAL, EF-HAND, BLOOD CLOTTING
1799	1dtl	A	183	306	1.4e-12	0.06	0.07		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1799	1dtl	A	241	379	8e-36	0.16	0.69		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1799	1exr	A	241	378	1.3e-44	0.13	0.12		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1799	1f71	A	247	309	8e-11	0.40	0.60		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1799	1f71	A	316	378	3.2e-24	0.44	0.16		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1799	1ff5	A	238	306	9.6e-10	0.25	0.21		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
1799	1ff5	A	313	379	1.3e-19	0.10	0.18		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
1799	1fpw	A	221	341	3.2e-15	0.18	0.03		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	METAL BINDING PROTEIN YEAST FREQUENTIN EF-HAND, CALCIUM LYASE GCAP-2; EF-HAND, CALCIUM-BINDING PROTEIN
1799	1jba	A	241	392	1.6e-29	0.46	0.99		GUANYLYLATE CYCLASE ACTIVATING PROTEIN 2;	

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1799	1tcf	232	378	3.2e-37	0.10	0.48			CHAIN-A;	GUANYLYL CYCLASE 2 REGULATION
1799	1tcf	233	379	3.2e-37					TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1799	1tnx	233	378	4.8e-36			63.35		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1799	1tnx	236	378	4.8e-36			61.69		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1799	1top	227	382	3.2e-38			0.05		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1799	1top	236	378	3.2e-38	0.02		64.51		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1799	1trc	A	242	306	6.4e-11	0.28	-0.05		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3 CALMODULIN (TR=2-CS) FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1799	1trc	A	314	378	1.1e-24	0.03	-0.09		CALCIUM BINDING PROTEIN CALMODULIN (TR=2-CS)	

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE D score	Compound	PDB annotation
1799	1virk	A	180	309	1.6e-14	-0.21	0.07		FRAGMENT COMPRISING RESIDUES 78 - 148 (TRC 3 OF THE INTACT MOLECULE) TRC 4	
1799	1virk	A	239	381	3.2e-46				CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	1virk	A	241	378	3.2e-46	0.12	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	1wdc	C	241	382	1.4e-20	0.23	0.04		SCAILOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1799	3ctn		238	306	9.6e-10	0.36	0.13		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
1799	3ctn		313	379	1.3e-19	0.19	0.12		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
1801	1alh	A	120	210	1.6e-12	0.03	0.35		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	158	238	4.8e-19	0.03	0.98		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1801	1alh	A	214	296	4.5e-37			84.50	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	270	377	1.1e-29	0.23	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	270	377	9.6e-22	-0.16	0.41		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	298	404	1.6e-19	0.22	0.57		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	298	454	3e-19	0.11	0.66		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	353	481	3e-21	0.07	0.78		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	382	481	3.2e-26	0.17	0.15		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	429	509	8e-30	0.45	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	429	510	9e-31	0.54	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE score	Compound	PDB annotation
									Oligonucleotide binding site; chain: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	457	537	1.1e-30	-0.09	1.00		QGSR zinc finger peptide; chain: A; duplex oligonucleotide binding site; chain: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1alh	A	485	565	7.5e-34	0.28	1.00		QGSR zinc finger peptide; chain: A; duplex oligonucleotide binding site; chain: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	1mey	C	119	210	8e-30	0.10	0.36		DNA; chain: A, B, D, E; consensus zinc finger protein; chain: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	157	238	1.4e-37	0.42	1.00		DNA; chain: A, B, D, E; consensus zinc finger protein; chain: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	185	266	3.2e-47	0.55	1.00		DNA; chain: A, B, D, E; consensus zinc finger protein; chain: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	213	294	3.2e-48	0.35	1.00		DNA; chain: A, B, D, E; consensus zinc finger protein; chain: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	241	322	4.8e-49	0.56	1.00		DNA; chain: A, B, D, E; consensus zinc finger protein; chain: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1801	1mey	C	241	323	4.8e-49		101.14	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA)
1801	1mey	C	269	377	4.8e-40	-0.06	0.51	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	297	453	1.1e-20	0.01	-0.17	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	353	481	1.3e-22	0.42	0.70	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	357	453	8e-41	0.41	0.24	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	381	481	3.2e-45	0.26	0.07	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	428	509	1.6e-49	0.51	1.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1801	1mey	C	456	537	1.6e-49	-0.03	0.99	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1mey	C	484	565	1.6e-49	0.25	1.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1801	1tfs	A	382	481	6.4e-17	0.23	-0.01	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIA; 5S GENE; NMR, TFIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 TRANSCRIPTION REGULATION/DNA)
1801	1tfs	A	112	247	1.4e-22	0.08	0.22	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1tfs	A	157	325	3e-61		114.65	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOLE score	Compound	PDB annotation
1801	1tf6	A *	158	303	9.6e-31	0.37	0.99	TFIIB; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1tf6	A	186	324	1.4e-35	0.15	1.00	TFIIB; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1tf6	A	298	495	1.3e-25	0.04	0.24	TFIIB; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1tf6	A	382	547	1.3e-34	-0.15	0.28	TFIIB; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1801	1tf6	A	429	565	1.6e-35	0.23	0.99	TFIIB; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQROL D score	Compound	PDB annotation
1801	1ubd	C	157	266	6e-43	0.25	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	159	267	7.5e-48		92.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	186	294	7.5e-48	0.35	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	217	322	7.5e-51	0.15	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1801	1ubd	C	221	322	1.6e-32	0.17	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)
1801	Iubd	C	249	377	3.2e-26	-0.16	0.99	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)	
1801	Iubd	C	305	453	1.6e-24	0.04	-0.02	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)	
1801	Iubd	C	351	509	1.5e-30	0.23	0.64	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)	
1801	Iubd	C	360	481	6.4e-29	0.26	0.36	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1801	1ubd	C	387	509	3.2e-31	0.07	0.65	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA) REGULATION(DNA)	
1801	1ubd	C	454	565	4.5e-40	0.30	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA)) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)	
1801	1ubd	C	464	565	8e-34	-0.10	0.98	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA)) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION(DNA)	
1801	2drp	A	294	377	3e-18	0.53	0.10	COMPLEX(TRANSCRIPTION REGULATION(DNA)) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3		

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOLE score	Compound	PDB annotation
1801	2gli	A	157	296	1.e-58			100.58	DNA 2DRP 4	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	157	296	3e-57	0.25	1.00		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	185	322	1.e-58	0.15	0.90		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	249	404	3.2e-23	0.01	0.81		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	297	511	1.e-37	0.11	0.49		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	360	508	8e-30	0.15	-0.02		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	424	536	6.4e-32	0.40	0.87		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	428	565	1.5e-48	0.25	0.75		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1801	2gli	A	436	564	1.e-33	0.39	0.69		ZINC FINGER PROTEIN GLI;	COMPLEX (DNA-BINDING

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1802	1afb	1	89	252	1.5e-21			59.81	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1802	1b68	A	118	249	3e-31	0.35	0.83		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
1802	1b6e		123	253	4.5e-29			74.73	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
1802	1b6e		126	251	4.5e-29	0.57	0.98		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
1802	1bj3	A	125	250	8e-25			67.59	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING HETERO-DIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPER-FAMILY, COLLAGEN BINDING PROTEIN
1802	1d88	A	103	249	1.2e-27	0.06	0.18		SURFACTANT PROTEIN A; CHAIN: A;	MEMBRANE PROTEIN SP-A; SP-A PHOSPHOLIPID MOLOLAYER COMPLEX
1802	1dv8	A	126	250	1.5e-28	0.47	1.00		ASIALOGLYCOPEPTIDE	SIGNALING PROTEIN IN HEPATIC
1802	1dv8	A	126	252	1.6e-28	0.35	0.48		RECEPTOR 1; CHAIN: A;	LECTIN H1; C-TYPE LECTIN CRD
1802	1e87	A	125	250	1.5e-27	0.79	0.65		ASIALOGLYCOPEPTIDE	SIGNALING PROTEIN IN HEPATIC
									RECEPTOR 1; CHAIN: A;	LECTIN H1; C-TYPE LECTIN CRD
									EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR
										ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1802	1hup		98	249	3e-27					RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR C-TYPE LECTIN ALPHA-HELICAL COILED-COIL IHUP 12
1802	1ixx	A	125	250	1e-24		63.07	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN; NULL; IHUP 5 COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER		
1802	1ixx	B	125	252	6e-25		65.37	COAGULATION FACTORS IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER		
1802	1lit		126	252	3e-25		61.47	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;		
1802	1qdd	A	114	252	3e-28	0.75	66.78	LITHOSTATHINE; CHAIN: A; NULL		PANCREATIC STONE INHIBITOR, LECTIN
1802	1qdd	A	114	252	3e-28	0.75	0.86	LITHOSTATHINE; CHAIN: A;		METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1802	1qdd	A	114	252	3e-28		74.13	LITHOSTATHINE; CHAIN: A;		METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1802	1qo3	C	123	253	1.5e-30	0.60	0.60	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D; LY49		COMPLEX (NK RECEPTOR/MHC CLASS I H-2 CLASS 1 HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE148, NK CEL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY49

SEQ NO:	PDB ID	CIAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1802	1q03	D	130	253	1.3e-27	0.81	0.43		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN YE1/48; NK CELL INHIBITOR RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49,	COMPLEX (NK RECEPTOR/MHC CLASS I H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL INHIBITOR RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49,
1802	1rdl	1	136	251	1.2e-26			61.44	MANNOSE-BINDING PROTEIN-C; 1RDL 6 CHAIN: 1, 2; 1RDL 7 LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20
1802	1rm	1	89	252	4.5e-23		-	63.45	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM 3 1RTM 96	
1802	2afp	A	123	250	1.3e-29	0.52	0.41		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1802	2msb	A	136	251	1.3e-25			61.86	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	
1803	1afb	1	127	291	1.5e-21			60.17	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1803	1b08	A	157	288	3e-31	0.35	0.83		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
1803	1b6e		162	292	4.5e-29			73.97	CD94; CHAIN: NULL;	BINDING PROTEIN NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN-LIKE, NKD
1803	1b6e		165	290	4.5e-29	0.57	0.98		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN-LIKE, NKD
1803	1b73	A	164	289	1e-24			68.01	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERO-DIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1803	1b73	A	165	288	1e-24	0.16	0.48		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERO-DIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1803	1c3a	B	165	290	4.5e-24	0.38	-0.06		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
1803	1du8	A	142	288	1.2e-27	0.06	0.18		SURFACTANT PROTEIN A; CHAIN: A;	MEMBRANE PROTEIN SP-A; SP-A:PHOSPHOLIPID MOLOGLAYER COMPLEX
1803	1dv8	A	165	288	4.8e-25	0.13	0.46		ASIALOGLYCOPEPTIDE RECEPTOR 1; CHAIN: A;	ASIALOGLYCOPEPTIDE RECEPTOR 1; CHAIN: A; SIGNALING PROTEIN HEPATIC LECTIN H1; C-TYPE LECTIN CRD
1803	1dv8	A	165	289	1.5e-28	0.47	1.00		ASIALOGLYCOPEPTIDE RECEPTOR 1; CHAIN: A;	ASIALOGLYCOPEPTIDE RECEPTOR 1; CHAIN: A; SIGNALING PROTEIN HEPATIC LECTIN H1; C-TYPE LECTIN CRD
1803	1e87	A	164	289	1.5e-27	0.79	0.65		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR (AM), EA 1, HEMATOPOIETIC CELL ACTIVATION INDUCER MOLECULE (AM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1803	legg	A	165	288	1.5e-25	0.62	0.95	MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	LECTIN-LIKE, 2 NKD, KLR SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
1803	lhup		150	288	3e-27		63.43	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5 COILED-COIL 1HUP 12	C-TYPE LECTIN ALPHA-HELICAL
1803	lhup		164	289	3e-27	0.33	0.40	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5 COILED-COIL 1HUP 12	C-TYPE LECTIN ALPHA-HELICAL
1803	l1xx	A	164	289	1e-24		65.74	COAGULATION FACTORS DDX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	l1xx	A	165	288	1e-24	0.32	0.48	COAGULATION FACTORS DDX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	l1xx	B	164	291	6e-25		61.53	COAGULATION FACTORS DDX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	l1it	B	165	290	6e-25	0.38	0.48	COAGULATION FACTORS DDX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING DDX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1803	l1it		165	291	3e-25	0.77	0.89	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
1803	l1it		165	291	3e-25		67.30	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
1803	1qdd	A	153	291	3e-28	0.75	0.86	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1803	1qdd	A	153	291	3e-28					PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1803	1qo3	C	162	292	1.5e-30	0.60	0.60	73.96	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1803	1qo3	D	169	292	1.3e-27	0.81	0.43			COMPLEX (NK RECEPTOR/MHC CLASS I H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK CELL SURFACE GLYCOPROTEIN YE148, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49)
1803	1rdl	1	175	290	1.2e-26			61.70	MANNOSE-BINDING PROTEIN-C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20
1803	1rdl	1	176	289	1.2e-26	0.41	0.70		MANNOSE-BINDING PROTEIN-C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1RDL 20
1803	1rm	1	127	291	4.5e-23			64.49	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1803	2afp	A	162	289	1.3e-29	0.52	0.41		3IRTM_96	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1803	2msb	A	175	290	1.3e-25			61.86	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	
1803	2msb	A	176	288	1.3e-25	0.57	0.54		LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	
1804	1auj	B	1	80	4.8e-24	0.10	0.87		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1804	1cdm	A	1	81	1.6e-29	-0.07	0.36		CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICIL 3
1804	1cll		1	81	8e-36	-0.04	0.49		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	
1804	1cmf		8	81	8e-32	0.23	0.60		CALMODULIN (VERTEBRATE); CALMODULIN 6 CHAIN; NULL; 1CMF 7 1CMF 9	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1804	1exr	A	1	81	9.6e-34	0.11	0.93		CALMODULIN; CHAIN: A;	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1804	1f71	A	14	81	8e-30	0.39	0.89		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1804	1tcf	I	1	81	1.6e-24	0.23	1.00		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1804	1top	I	1	81	1.6e-24	0.25	0.95			CONTRACTILE SYSTEM
1804	1trc	A	12	81	1.4e-30	0.52	0.98		PROTEIN TROPONIN C 1TOP 3 CALCIUM BINDING PROTEIN CALMODULIN (TR=2-CS FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1804	1vrik	A	1	82	3.2e-35	0.30	0.98		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN PEPTIDE)
1805	1a9n	A	114	250	8e-24	0.60	1.00		U2 RNA HAIRPIN IV; CHAIN: Q; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1805	1a9n	C	114	250	8e-24	0.58	0.99		U2 RNA HAIRPIN IV; CHAIN: Q; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1806	1d0b	A	44	227	6.4e-34	0.57	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1806	1d0b	A	92	235	1.3e-32	0.39	1.00		INTERNAL B; CHAIN: A;	ADHESION
1806	1dee	A	132	249	3.2e-25	0.51	0.99	RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	
1806	1dee	A	84	207	3.2e-17	0.45	0.88	RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	
1806	1ds9	A	111	191	3e-14	-0.40	0.78	OUTER ARM DYNEIN; CHAIN: A;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	
1806	1ds9	A	125	251	1.6e-28	-0.60	0.46	OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	
1806	1ds9	A	73	179	3.2e-13	-0.30	0.01	OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	
1809	1dkg	A	250	398	0.0015	-0.10	0.11	NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B; MOLECULAR CHAPERONE	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE EXCHANGE 2	

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1809	1dnl	B	143	367	3e-08	0.06	-0.07	DNAK; CHAIN: D;	FACTOR, COILED-COIL, COMPLEX (HSP24/HSP70)
1809	1quu	A	102	374	7.5e-13	-0.12	0.07	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT CONTRACTILE PROTEIN TRIPLE-Helix COILED COIL.
1812	1ses	A	439	528	1.6e-05	0.21	0.28	HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN
1814	1qhw	A	32	310	4.5e-10			LIGASE(SYNTETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4	LIGASE(SYNTETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4
1814	1qhw	A	39	239	4.5e-10	-0.19	0.34	PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A;
1814	1ute	A	28	320	0.00014			PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A;
1814	4kbp	A	10	247	1.5e-12	0.01	0.52	PURPLE ACID PHOSPHATASE; CHAIN: A, B, C, D;	PAP, TARTRATE RESISTANT ACID PURPLE ACID PHOSPHATASE, TARTRATE RESISTANT ACID 2 PHOSPHATASE, METALLOENZYME, UTEROFERRIN, HYDROLASE HYDROLASE (PHOSPHORIC MONOESTER) (PHOSPHORIC MONOESTER)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1815	1b7f	A	195	272	3.2e-05	-0.30	0.46		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-CHAIN: P, Q; COMPLEX	RNA-BINDING PROTEIN; PRE-MRNA; SPlicing REGULATION; RNP DOMAIN; RNA COMPLEX
1815	1fjc	A	180	250	9.6e-09	-0.15	0.12		NUCLEOLIN RBD2; CHAIN: A; C23; RNP; RBD; RRM; RNA BINDING DOMAIN; NUCLEOLUS	STRUCTURAL PROTEIN PROTEIN C23; RNP; RBD; RRM; RNA BINDING DOMAIN; NUCLEOLUS
1815	1mr8	A	101	149	0.0045	0.07	0.21		MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	METAL TRANSPORT MRP8, S100A8, CALGRANULIN A CALCIUM-BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR - RELATED PROTEIN 8, S100 PROTEIN
1815	1sxj		195	272	3.2e-05	-0.32	0.13		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN IC-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	RNA-BINDING PROTEIN SEX-LETHAL PROTEIN IC-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5
1815	2u1a		188	267	0.003	0.29	0.55		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEAR PROTEIN U1 SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
1815	2u1a		195	256	0.0093	0.31	0.31		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEAR PROTEIN U1 SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
1815	3sxj	A	195	257	6.4e-05	-0.10	0.18		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DOSAGE COMPENSATION
1819	1ekl	A	172	305	3.2e-09	-0.00	-0.14		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1819	1ekl	B	39	69	0.006	-0.84	0.03		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1819	1fz2	A	38	143	9e-06	0.20	0.64		PHOSPHONOACETALDEHYDE HYDROLASE; CHAIN: A, B, C, D;	HYDROLASE HAD-FAMILY ALPHA/BETA CORE DOMAIN, MGII) BINDING SITE, 5- 2 HELIX BUNDLE
1819	1zm		28	316	3e-10	0.12	-0.19		L-2-HALOACID DEHALOGENASE; CHAIN: NULL;	DEHALOGENASE DEHALOGENASE, HYDROLASE
1820	1bc6		137	219	8e-14	0.05	-0.19		7-Fe FERREDOXIN; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR
1820	1bc6		176	254	1.1e-10	0.17	-0.17		7-Fe FERREDOXIN; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR
1820	1clf		137	199	1.1e-10	0.43	-0.17		FERREDOXIN; ICLF 5 CHAIN; NULL, ICLF 6	ELECTRON TRANSFER (IRON-SULFUR PROTEIN)
1820	1dur	A	137	200	1.6e-11	0.53	-0.12		[214Fe-4S] FERREDOXIN; CHAIN: A	ELECTRON TRANSPORT TWO 4Fe-4S CLUSTERS
1820	1e08	A	136	519	6.4e-68	0.37	1.00		[Fe]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [Fe]-HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
1820	1e08	A	173	504	3e-92	0.23	1.00		[Fe]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [Fe]-HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
1820 1fsh	A	1	574	1.4e-85			232.77	PERPLASMIC HYDROGENASE I; CHAIN: A;	OXIDOREDUCTASE
1820 1fsh	A	69	572	1.4e-85	0.33	1.00		PERPLASMIC HYDROGENASE I; CHAIN: A;	OXIDOREDUCTASE
1820 1hfe	L	117	524	4.5e-92			223.69	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S; T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L; M;	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERPLASM
1820 1hfe	L	122	519	3.2e-68	0.40	1.00		FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S; T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L; M;	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERPLASM
1820 1hfe	L	173	504	4.5e-92	0.61	1.00		FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S; T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L; M;	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERPLASM
1821 1cun	A	104	344	6e-09	-0.18	0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1821 1cun	A	51	207	1.5e-07	-0.09	0.36		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1821 1quu	A	54	302	9e-12			52.84	HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1821 1quu	A	56	340	9e-12	-0.34	0.43		HUMAN SKELETAL MUSCLE	CONTRACTILE PROTEIN TRIPLE-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									ALPHA ACTININ 2; CHAIN: A;	HELIX COILED COIL, CONTRACTILE PROTEIN
1822	1aut	L	29	125	9e-08		51.57		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MA; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIa; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1822	1bx7		45	113	6e-11	1.12	-0.15		HIRUSTASIN; CHAIN: NULL;	ANTI-COAGULANT ANTI- COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR
1822	1c2a	A	36	165	1.4e-26	0.53	-0.03		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1822	1c2a	A	4	126	1.5e-19	0.87	-0.15		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1822	1dan	L	2	135	7.5e-13	0.56	-0.19		BLOOD COAGULATION FACTOR VIIa; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DPFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1822	1du3	A	2	77	7.5e-11	1.08	-0.18		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	APOPTOSIS TRAIL, DR5, COMPLEX
1822	1du3	A	31	125	4.5e-12	0.59	-0.12		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED	APOPTOSIS TRAIL, DR5, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1822	1du3	A	9	96	6e-12	1.17	-0.15	APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, I, K, L; DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, I, K, L;	APOPTOSIS TRAIL, DR5, COMPLEX
1822	1dx5	I	47	155	4.5e-11	0.58	-0.14	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARGIN; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGFR-CMVK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTIKOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1822	1ehd	A	12	111	1.4e-18	0.49	-0.18	AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEN-LIKE DOMAINS
1822	1ehd	A	4	91	7.5e-19	1.11	-0.12	AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEN-LIKE DOMAINS
1822	1ehd	A	52	141	1.4e-18	1.00	0.16	AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEN-LIKE DOMAINS
1822	1eis	A	19	121	1.5e-19	0.87	0.17	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1822	1eis	A	4	90	1.2e-19	1.02	-0.11	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1822	1eis	A	52	141	1.5e-19	1.08	0.10	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1822	1eis	A	75	160	7.5e-17	0.24	-0.17	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1822	1en2	A	12	121	3e-18	0.40	-0.13	CHAIN: A;	SUPERANTIGEN
1822	1en2	A	2	90	6e-16	1.10	-0.18	AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVENV DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1en2	A	52	141	3e-21	1.04	0.11	AGGLUTININ ISOLECTIN V/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVENV DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1en2	A	62	160	6e-18	0.61	-0.14	AGGLUTININ ISOLECTIN V/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVENV DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	1ext	A	10	177	7.5e-20		62.34	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A; B;	RECEPTOR, CYTOKINE, SIGNALLING PROTEIN
1822	1ext	A	12	175	7.5e-20	0.78	-0.14	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A; B;	RECEPTOR, CYTOKINE, SIGNALLING PROTEIN
1822	1ext	A	3	128	6e-13	0.63	-0.14	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A; B;	RECEPTOR, CYTOKINE, SIGNALLING PROTEIN
1822	1igr	A	4	178	1.5e-28	0.40	-0.19	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE FAMILY
1822	1klo	47		178	1.2e-19	0.65	-0.15	LAMMIN; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1klo	4	155	7.5e-27	1.13	-0.06		LAMMIN; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1klo	4	157	7.5e-27			82.39	LAMMIN; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1ncf	A	34	171	1.5e-12		50.41	TUMOR NECROSIS FACTOR RECEPTOR; INCN 4 CHAIN: A,	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFRI; INCN 8

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOLD D score	Compound	PDB annotation
1822	1ncf	A	35	155	1.5e-12	0.68	-0.14		B; 1NCF 5	BINDING PROTEIN, CYTOKINE 1NCF 19
1822	1nub	A	12	171	6e-26	0.10	-0.19		TUMOR NECROSIS FACTOR RECEPTOR; 1NCF 4 CHAIN: A, B; 1NCF 5	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; 1NCF 8 BINDING PROTEIN, CYTOKINE 1NCF 19
1822	1px	L	19	179	3e-23	0.14	-0.20		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	EXTRACELLULAR MODULE OSTEONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES
1822	1px	L	36	178	3e-23				FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1822	1px	L	3	123	9e-14	0.44	-0.20		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1822	1skz			22	134	1.2e-18	0.63	0.54	ANTISTASIN; CHAIN: NULL;	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN SERINE PROTEASE INHIBITOR
1822	1skz			43	147	7.5e-21	0.57	-0.06	ANTISTASIN; CHAIN: NULL;	FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR
1822	1skz			71	176	7.5e-25	0.03	0.11	ANTISTASIN; CHAIN: NULL;	FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR
1822	1skz			71	180	7.5e-25		63.90	ANTISTASIN; CHAIN: NULL;	FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR
1822	1skz			8	117	1.5e-18	0.61	-0.12	ANTISTASIN; CHAIN: NULL;	FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										INHIBITOR, THROMBOSIS
1822	9wga	A	2	158	6e-30			107.39	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1822	9wga	A	2	160	3e-26	0.57	0.03		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1824	1bx7		50	107	4.5e-20	0.23	0.07			
1824	1du3	A	49	107	3e-08	0.07	-0.12		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L; METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MHUA 2	ANTI-COAGULANT ANTI-COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR APOPTOSIS TRAIL, DR5, COMPLEX
1824	1mhu		78	108	9e-16	0.40	1.00			
1824	1mhu		78	108	9e-16			65.07	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MHUA 2	
1824	1mr1		78	108	9e-16	0.49	1.00		METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MRLA 2	
1824	1mr1		78	108	9e-16			63.47	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MRLA 2	
1824	1xka	L	54	106	7.5e-06	0.34	0.10		BLOOD COAGULATION FACTOR XA; CHAIN: L, C; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
1824	4mt2	48	108	1.3e-14	-0.09	0.15		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1824	4mt2	48	108	1.3e-14			127.57	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1825	1a25	A	355	491	4.8e-42	0.47	1.00	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM+-PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1825	1a25	A	528	646	3.2e-37	0.27	0.90	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM+-PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1825	1bor		60	109	0.00075	0.33	0.13	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1825	1byn	A	355	484	3.2e-46	0.68	1.00	SYNAPTOTAGMIN I; CHAIN: A; SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1825	1byn	A	510	639	1.4e-27	0.70	0.98	SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2 DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1825	1cij	A	366	480	1.1e-12	0.17	0.01	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1825	1cij	A	526	639	1.2e-15	0.37	0.28	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING,

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1825	1dix	A	370	467	4.5e-15	0.19	0.62		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE
1825	1dix	A	326	620	6e-13	-0.07	0.12		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1825	1dix	B	370	467	4.5e-15	0.16	0.58		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1825	1dqv	A	357	649	3.2e-88	0.47	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA DOMAIN SANDWICH, CALCIUM ION, C2
1825	1dqv	A	512	671	4.8e-33	0.24	0.46		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA DOMAIN SANDWICH, CALCIUM ION, C2
1825	1dsy	A	354	494	1.3e-45	0.33	0.96		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++; PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1825	1dsy	A	510	650	6.4e-40	0.38	0.31		PROTEIN KINASE C, ALPHA	TRANSFERASE CALCIUM++,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1825	1g25	A	60	109	0.00045	0.10	0.10		TYPE; CHAIN: A;	PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1825	1rlw								CDK ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
1825	1rlw		373	480	1.5e-16	-0.18	0.41		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1825	1rlw		528	631	7.5e-17	0.31	0.23		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1825	1rmrd		40	109	0.003	0.21	0.03		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1825	1rsy		347	483	4.8e-46			81.61	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1825	1rsy		355	482	4.8e-46	0.81	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1825	1rsy		510	636	1.6e-27	0.48	0.96		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1825	1rvfy	A	60	91	0.00075	0.04	0.16		PHOSPHATIDYL INOSITOL-3-PHOSPHATE BINDING FYVE	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1825	1zbd	B	10	120	3e-22	0.40	0.69		CHAIN: A;	MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN COMPLEX (GTP-)
1825	1zbd	B	8	131	3e-22				RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN-EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1825	3rpb	A	357	496	3.2e-29	0.62	1.00		71.27 RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN-EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1825	3rpb	A	512	649	1.4e-46	0.53	0.58		RABPHILIN-3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1828	1cll		29	169	4.8e-53			69.53 ICLL ₃	CALMODULIN (VERTEBRATE)	
1828	1vfk	A	26	170	1.1e-60			72.01 RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1833	1aut	L	47	145	1.3e-20			58.73	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN II A; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1833	1aut	L	73	202	1.3e-20	0.14	-0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN II A; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1833	1dan	L	152	231	6.4e-16	0.10	0.96		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYL KETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1833	1dan	L	54	193	1.5e-22			60.57	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYL KETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1833	1dva	L	152	231	6.4e-16	0.26	0.99		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1833	lenn		149	226	1.3e-15		56.72	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1833	1ext	A	10	173	9e-14		54.06	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A; B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1833	1fak	L	152	231	6.4e-16	0.44	1.00	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: L;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1833	1ki0		43	205	1e-28	0.32	0.43	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1833	1ki0		95	242	1.1e-20	0.12	-0.01	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1833	1ki0		95	247	1e-28		70.82	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1833	1px	L	22	146	6e-35		64.61	FACTOR IXA; CHAIN: C; L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1833	1px	L	54	218	6e-35	0.10	-0.12	FACTOR IXA; CHAIN: C; L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1833	1pfk	L	92	226	6e-29	-0.16	0.07	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1833	1qfk	L	156	226	1.5e-21	0.07	0.62	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPePTIDYL INHIBITOR; CHAIN: C;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1833	1qfk	L	156	231	6.4e-15	0.30	0.98	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPePTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1833	1qfk	L	91	195	7.5e-24			COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPePTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1833	1qfk	L	92	207	7.5e-24	0.04	0.18	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
									(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
1833	1tpg		137	226	1e-23	-0.02	0.63		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1833	1tpg		43	125	1e-23	0.27	0.19		F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1833	1tpg		72	196	3e-21	0.23	0.16		F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1833	1vap	A	34	130	4.5e-18	0.03	-0.12		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2; LIPID DEGRADATION, HYDROLASE
1833	1xka	L	156	226	3e-18	0.18	0.64		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
1833	1xka	L	91	208	1.1e-21			59.27	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
1833	1xka	L	92	207	1.1e-21	0.32	0.06		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2
1833	9wga	A	28	207	7.5e-25			78.80	LECTIN (AGGLUTinin) WHEAT GERM AGGLUTinin (ISOLECTIN 2) 9WGA 3	GROWTH FACTOR LIKE DOMAIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1834	1f88	A	4	320	3e-20	0.11	-0.07		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1834	1f88	B	4	299	7.5e-18	-0.14	0.10		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1835	1b7f	A	61	144	1.6e-19	-0.03	0.36		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)-3'). CHAIN: P, Q; COMPLEX N-4 CYTOSINE-SPECIFIC TRANSFERASE TYPE II DNA-METHYLTRANSFERASE FVU II; CHAIN: A;	RNA-BINDING PROTEIN/RNA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1835	1bo0	A	433	480	4.5e-05	-0.57	0.27			(CYTOSINE N4) METHYLTRANSFERASE, AMINO 2 METHYLATION, SELENOMETHIONINE, MULTIWAVELENGTH ANOMALOUS 3 DIFFRACTION
1835	1cvj	A	59	150	6.4e-23	-0.34	0.24		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1835	1cvj	B	75	237	3.2e-26	0.05	-0.19		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1835	1d2h	A	424	492	1.2e-14	-0.57	0.17		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1835	1d9a	A	72	144	3.2e-17	-0.02	0.16		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1835	1dus	A	421	567	9.6e-20	0.37	0.75		M10882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1835	1fjc	A	73	139	1.3e-13	0.19	0.62		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1835	1g6q	I	402	580	3.2e-11	-0.51	0.03		HNRP ARGINTINE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1g6q	I	420	492	1.3e-13	0.20	0.83		HNRP ARGINTINE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1hd1	A	74	144	3.2e-23	0.27	0.06		HETEROGENEous NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1835	1qam	A	410	592	6e-21	-0.06	0.58	ERM'C	METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RNA MethylTRANSFERASE ERMC', COFACTOR ANALOGS
1835	1qam	A	413	524	6.4e-05	-0.12	0.05	ERM'C	METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RNA MethylTRANSFERASE ERMC', COFACTOR ANALOGS
1835	1wid							CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE,	
1835	1xva	A	426	492	1.5e-10	-0.47	0.05		GLYCINE N-METHYLTRANSFERASE;	METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
										METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE;

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1835	2mss	A	74	144	4.8e-18	-0.04	0.00	CHAIN: A, B; MUSASHI; CHAIN: A;	GLYCINE METHYLTRANSFERASE RNA BINDING PROTEIN RNA-BINDING DOMAIN
1835	2szl		73	152	8e-18	0.04	0.35	SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPlicing
1835	3sxl	A	61	137	8e-18	0.10	-0.05	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA-BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1836	1buo	A	4	85	3.2e-16	0.37	-0.05	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN, PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER - PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1836	1gof								
1836	1gof		204	505	1.6e-06	-0.33	0.34	OXIDOREDUCTASE(OXY GEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9)(PH 4.5) 1GOF 3	
1836	1gof		217	450	7.5e-13	-0.42	0.13	OXIDOREDUCTASE(OXY GEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9)(PH 4.5) 1GOF 3	
1836	1gof		246	372	1.5e-15	-0.23	0.07	OXIDOREDUCTASE(OXY GEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9)(PH 4.5) 1GOF 3	
1837	1dan	L	285	370	4.8e-10	-0.00	-0.20	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1837	1dan	L	361	449	1.1e-12	0.04	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1837	1dan	L	530	583	3.2e-08	0.21	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1837	1dva	L	285	370	4.8e-10	0.09	-0.20		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M, (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1837	1dva	L	361	449	1.1e-12	0.10	-0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M, (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1837	1dva	L	530	583	3.2e-08	0.27	-0.20		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M, (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1837	1emn	*	107	185	1.4e-10	0.19	-0.19	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1837	1emn		149	227	3.2e-09	0.07	-0.17	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1837	1emn		530	583	4.8e-09	0.03	-0.20	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1837	1f5y	A	102	182	1.6e-11	0.03	-0.20	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
1837	1f5y	A	143	221	4.8e-09	0.13	-0.20	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
1837	1fak	L	530	583	3.2e-08	0.22	-0.20	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE(COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T; 5LJ5; CHAIN: I;	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1837	1pfx	L	328	409	1.1e-12	0.22	-0.13		FACTOR IXA; CHAIN: C, L.; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1837	1pfx	L	361	449	1.6e-11	0.16	-0.19		FACTOR IXA; CHAIN: C, L.; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1837	1qfk	L	152	243	4.8e-10	0.03	-0.15		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRipeptidyl INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1837	1qfk	L	365	449	6.4e-12	0.02	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRipeptidyl INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1837	1qfk	L	550	583	3.2e-08	0.08	-0.20		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
1837	1vmo	A	303	470	3e-15	0.19	-0.19		(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE
1837	1xka	L	530	585	1.6e-08	0.22	-0.20		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO3	
1837	1xka	L	73	158	4.8e-11	0.04	-0.20		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1837	9wga	A	250	403	9.6e-16	0.21	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) SWGA 3	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1837	9wga	A	275	476	4.8e-16	0.01	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) SWGA 3	
1838	1a7a	A	163	207	0.0032	-0.09	0.00		S-ADENOSYLHOMOCYSTEINE HYDROLASE; CHAIN: A, B;	HYDROLASE HYDROLASE, NAD BINDING PROTEIN
1838	1ael	A	173	215	0.00064	0.34	0.21		TROPINONE REDUCTASE I; CHAIN: A, B;	OXIDOREDUCTASE, TROPANE- ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1838	lael	B	173	215	0.00064	0.44	0.05		TROPINONE REDUCTASE; I; CHAIN: A, B;	OXIDOREDUCTASE, TROPANE OXIDOREDUCTASE, TROPINE, SHORT-CHAIN DEHYDROGENASE
1838	1bdb								CIS-BIPHENYL-2,3-DIHYDRODIOL-2,3-DEHYDROGENASE; CHAIN: NULL;	REDUCTION OF 2 TROPINONE TO DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION
1838	lcld	A	173	221	0.00013	0.67	0.89		L-PHENYLALANINE DEHYDROGENASE; CHAIN: A; L-PHENYLALANINE DEHYDROGENASE; CHAIN: B;	OXIDOREDUCTASE AMINO ACID DEHYDROGENASE, OXIDATIVE DEAMINATION MECHANISM, 2
1838	1cdo	A	1	367	1.3e-76			56.21	ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; 1CDO 7	OXIDOREDUCTASE (CH-OHD)-NAD(A) OXIDOREDUCTASE 1CDO 15
1838	1cdo	A	25	366	1.3e-76	0.64	1.00		ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; 1CDO 7	OXIDOREDUCTASE (CH-OHD)-NAD(A) OXIDOREDUCTASE 1CDO 15
1838	1cyd	A	173	261	3.2e-05	0.19	0.03		CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
1838	1dit	A	1	367	4.8e-75			64.19	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DNucleotide-fold
1838	1dit	A	26	366	4.8e-75	0.81	1.00		ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DNucleotide-fold
1838	1deh	A	25	366	3.2e-81	0.63	1.00		HUMAN BETA ALCOHOL DEHYDROGENASE; IDEH 7	OXIDOREDUCTASE BETAI ADH; IDEH 9 NAD+ DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1838	1deh	A	3	367	3.2e-81				CHAIN: A, B; IDEH 8	ALCOHOL DEHYDROGENASE IDEH 26
							74.95		HUMAN BETA 1 ALCOHOL DEHYDROGENASE; IDEH 7	OXIDOREDUCTASE BETA 1 ADH; IDEH 9 NAD+ DEPENDENT
									CHAIN: A, B; IDEH 8	ALCOHOL DEHYDROGENASE IDEH 26
1838	1e3j	A	26	366	1.6e-69	0.77	1.00		ALCOHOL DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE, ALCOHOL DEHYDROGENASE
1838	1ee2	A	25	366	4.8e-77	0.73	1.00		ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DEHYDROGENASE, ALCOHOL, NICOTINAMIDE COENZYME, STEROID 2 BINDING
1838	1hdc	A	173	284	9.6e-07	-0.03	0.45		OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) 1HDC 3 COMPLEXED WITH CARBENOXOLONE 1HDC 4	OXIDOREDUCTASE DEHYDROGENASE, CHAIN: A, B, C, D; NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D.
1838	1kev	A	24	369	1.6e-51			53.09	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D.	OXIDOREDUCTASE, ZINC, NADP OXIDOREDUCTASE, ZINC, NADP
1838	1kev	A	50	367	1.6e-51	0.59	1.00		NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D.	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP
1838	1qo8	A	168	207	0.0032	0.28	0.47		FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1838	1qor	A	37	370	8e-70			116.09	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE QUINONE COMPLEXED WITH NADPH 1QOR 3	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH
1838	1qor	A	38	367	8e-70	0.75	1.00			

SEQ NO.	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1838	lteh	A	1	367	1.6e-86		72.11		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD ⁺ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
1838	lteh	A	27	366	1.6e-86	0.60	1.00		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD ⁺ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
1838	1vid		164	268	0.0009	0.51	0.47		CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
1838	lybv	A	173	280	9.6e-05	-0.20	0.49		TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE, OXIDOREDUCTASE
1838	lykf	A	24	370	4.8e-54			52.30	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1838	lykf	A	52	367	4.8e-54	0.56	1.00		NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1839	1a06		71	349	9.6e-09			52.68	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1839	1b6c	B	50	350	1.1e-15		58.79	CHAIN: NULL; FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H; RECEPTOR 2 SERINE/THREONINE KINASE	CALCIUM/CALMODULIN COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1839	1b6c	B	70	199	1.5e-13	-0.17	0.06	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H; RECEPTOR 2 SERINE/THREONINE KINASE	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1839	1byg	A	73	337	3.2e-27		62.45	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2; STAUROSPORINE, TRANSFERASE
1839	1byg	A	78	197	1.5e-13	-0.33	0.00	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2; STAUROSPORINE, TRANSFERASE
1839	1byg	A	87	334	3.2e-27	-0.39	0.01	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2; STAUROSPORINE, TRANSFERASE
1839	1fgk	A	64	339	1.1e-26		70.22	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1839	1fgk	B	63	338	3.2e-26		71.37	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	
1839	1fgk	B	87	335	3.2e-26	0.11	0.41	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	
1839	1fpu	A	84	332	1.6e-27	-0.20	0.10	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571 ACTIVATION LOOP	
1839	1hcl	79	321	1.4e-22	-0.13	0.33		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	
1839	1i3	A	63	350	3.2e-26		61.82	INSULIN RECEPTOR, CHAIN: A; PEPTIDE SUBSTRATE, CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	
1839	1i3	A	87	332	3.2e-26	0.10	0.16	INSULIN RECEPTOR, CHAIN: A; PEPTIDE SUBSTRATE, CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B;	TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1839	1qcf	A	84	347	1.1e-24	-0.26	0.29		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP TRANSFERASE KDR; TYROSINE KINASE
1839	1vr2	A	87	336	1.6e-20	-0.38	0.03		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	
1840	1c1g	A	2	176	8e-09	0.14	-0.20		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1840	1req	A	2	164	1.3e-08	0.19	-0.13		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D; TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP23, PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1840	2hrc	P	6	112	4.5e-09	0.53	-0.19			
1841	1alh	A	117	191	8e-23	-0.46	0.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFFOL D score	Compound	PDB annotation
1841	lalh	A	166	249	6.4e-30			Oligonucleotide binding site; chain: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1841	lalh	A	167	247	6.4e-30	-0.18	0.93	QGSR zinc finger peptide; chain: A; duplex oligonucleotide binding site; chain: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	lalh	A	195	281	3.2e-26	0.06	0.25	QGSR zinc finger peptide; chain: A; duplex oligonucleotide binding site; chain: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	lalh	A	325	400	6.4e-24	-0.34	0.33	QGSR zinc finger peptide; chain: A; duplex oligonucleotide binding site; chain: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	lalh	A	348	428	6.4e-30	-0.66	0.87	QGSR zinc finger peptide; chain: A; duplex oligonucleotide binding site; chain: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1841	lard							Transcription regulation factor Adr1 (amino terminal zinc finger domain) (NMR 10 structures) IARD 4 (ADR1B) IARD 5	
1841	lmey	C	109	191	1.6e-38	-0.12	0.22	DNA; chain: A, B, D, E; consensus zinc finger protein; chain: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1841	1mey	C	138	219	1.6e-47	-0.01	0.98	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	C	166	247	1.6e-48	0.11	1.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	C	166	248	1.6e-48			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	C	194	282	8e-45	-0.14	0.22	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	C	324	400	1.1e-41	-0.60	0.22	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	C	347	428	1.6e-45	-0.19	0.82	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	G	220	247	1.1e-12	0.13	0.70	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA. INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB
1841	1mey	G	345	372	6.4e-13	-0.26	0.95			CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1mey	G	401	428	1.6e-13	0.03	0.48	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1841	1sp2		348	376	8e-09	-0.21	0.03	SPI1F2; CHAIN: NULL;		ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI
1841	1t3	A	195	267	1.1e-20	0.03	-0.11	TRANSRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;		COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1841	1t6	A	112	278	3.2e-33		74.20	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;		COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1t6	A	139	284	3.2e-33	-0.25	0.49	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;		COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	PsiBlast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1841	1if6	A	297	437	4.8e-31	-0.30	0.19		TFIILA; CHAIN: A; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1if6	A	348	488	6.4e-34	-0.37	0.04		TFIILA; CHAIN: A; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1841	1ubd	C	109	219	3.2e-30	-0.16	0.19		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	1ubd	C	140	248	3e-32			77.97	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1841	1ubd	C	143	247	3e-32	-0.33	0.78		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF D score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (TRANSCRIPTION(DNA))
1841	1ubd	C	174	281	3.2e-32	-0.25	0.04		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (TRANSCRIPTION(DNA))
1841	1ubd	C	332	428	6.4e-30	-0.46	0.40		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (TRANSCRIPTION(DNA))
1841	2drp	A	323	371	4.8e-06	-0.52	0.01		COMPLEX(TRANSCRIPTION REGULATION(DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	COMPLEX(TRANSCRIPTION REGULATION(DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4
1841	2gii	A	138	283	1.6e-32				ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN(DNA) FIVE-FINGER GLI; GL, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN(DNA))
1841	2gii	A	140	252	6e-29	-0.12	0.62		ZINC FINGER PROTEIN GLII;	COMPLEX (DNA-BINDING

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1841	2gli	A	146	283	1.6e-32	0.09	-0.05	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1845	1cun	A	511	648	1.5e-09	1.09	-0.17	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1845	1cun	A	566	798	7.5e-05	0.39	0.00	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1845	1dn1	B	437	613	4.5e-10	0.41	-0.20	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1845	1dn1	B	481	642	1.5e-17	0.57	-0.20	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1845	1dn1	B	513	769	1.5e-11	0.43	-0.17	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1845	1ez3	A	447	576	1e-09	0.78	-0.19	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1845	1ez3	A	485	601	3e-16	0.83	-0.19	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	SEQFOOL D score	Compound	PDB annotation
1845	1ez3	A	511	630	1.5e-16	1.11	-0.20	SYNTAXIN-1A; CHAIN: A, B, C;	BUNDLE
1845	1ez3	A	526	658	3e-16	0.98	-0.17	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1845	1ez3	A	739	861	4.5e-05	0.21	0.00	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1845	1f5n	A	485	626	3e-08	0.74	-0.19	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALLING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPNNP, GPPNHP.
1845	1fio	A	485	642	9e-13	0.55	-0.20	SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1845	1guu	A	460	656	3e-24	0.70	-0.19	HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1845	1req	A	451	746	4.5e-31	0.48	-0.08	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
1845	1sig		485	643	4.5e-18	0.76	-0.15	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION
1845	1sig		486	677	6e-17	0.40	-0.20	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1845	2rc	P	488	621	1.5e-17	0.22	-0.20	TRANSDUCIN; CHAIN: B, G;	TRANSCRIPTION REGULATION COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
		*							PHOSDUCIN; CHAIN: P;	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA; PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1845	2irc	P	513	647	1.5e-20	0.29	-0.19		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA; PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1845	2irc	P	577	746	1.5e-13	0.23	-0.20		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA; PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1849	1bor		29	55	1.1e-07	-0.68	0.59		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQOFOL D score	Compound	PDB annotation
1849	1ksr		397	500	4.5e-30			64.85	GELATION FACTOR; CHAIN: NULL;	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120
1849	1ksr		398	498	4.5e-30	0.47	0.99		GELATION FACTOR; CHAIN: NULL;	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120
1849	1ksr		398	499	1.3e-19	0.54	1.00		GELATION FACTOR; CHAIN: NULL;	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120
1849	1qfh	A	306	515	6e-36			62.06	GELATION FACTOR CHAIN: A, B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1849	1qfh	A	359	494	1.6e-13	0.11	0.95		GELATION FACTOR; CHAIN: A, B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1849	1qfh	A	395	528	1.3e-19	0.52	0.96		GELATION FACTOR; CHAIN: A, B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1849	1qfh	A	397	528	6e-36	0.52	0.99		GELATION FACTOR; CHAIN: A, B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120
1850	1d2h	A	175	331	7.5e-06	-0.00	0.21		GLYCINE N-	TRANSFERASE

SEQ NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1850	1dus	A	177	294	6.4e-09	0.24	0.01	METHYLTRANSFERASE; CHAIN: A, B, C, D; MJ0882; CHAIN: A;	METHYLTRANSFERASE
1850	1g6q	1	148	292	1.3e-14	0.11	0.04	FNRNP ARGININE-N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHI TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1853	1a5e			538	668	4.5e-32	0.39	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1853	1apm	E	1	349	4.5e-30		99.80	TRANSFERASE (PHOSPHOTRANSFERASE) SC-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC1APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PRK(5'-24) AND THE DETERGENT MEGA-8 1APM 6 GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	
1853	1awc	B	447	604	1.5e-36	0.33	1.00		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHABETA1; COMPLEX (TRANSCRIPTION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION FACTOR
1853	1awc	B	486	637	7.5e-43	0.55	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHABETA1; COMPLEX

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1853	1awc	B	551	705	1.2e-45				DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING,
1853	1awc	B	556	704	6.4e-35	0.72	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	
1853	1awc	B	584	737	1.2e-45	0.70	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	
1853	1awc	B	617	770	1.5e-44	0.60	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
1853	lawc	B								2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	lawc	B	651	802	1.5e-42	0.63	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	lawc	B	656	802	1.6e-32	0.34	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	lawc	B	667	828	3e-35	0.74	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1853	1b6c	B	26	276	3e-49	0.37	1.00	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE 1; CHAIN: B, D, F, H;		COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/TREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/TREONINE KINASE

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1bd8		445	574	4.8e-10	0.37	0.49		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8	*	458	605	4.5e-35	0.66	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		486	637	1.4e-40	0.58	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		518	673	1.5e-44	0.76	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		585	739	6e-42	0.32	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bd8		652	805	1.5e-40	0.51	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1853	1bix	B	447	610	1.1e-36	0.21	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bix	B	521	673	3e-43	0.77	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,
1853	1bix	B	587	743	1.5e-41	0.63	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,

SEQ ID NO.	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1bix	B	651	808	4.5e-41	0.60	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P18INK4D; CHAIN: B;	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bu9	A	444	576	8e-09	0.16	0.87		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1853	1bu9	A	486	612	4.5e-33	0.60	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1853	1byg	A	24	276	1.4e-45	0.81	0.98		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2-STAUROSPORINE, TRANSFERASE
1853	1cmk	E	1	349	1.5e-30			96.05	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1853	1cip	E	1	342	1.5e-30			92.53	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1853	1d9s	A	478	610	1e-35	0.73	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1d9s	A	510	637	1.5e-33	0.36	1.00		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1853	1d9s	A	545	673	7.5e-38	0.65	1.00	4 INHIBITOR B; CHAIN: A;	HELIX, ANKYRIN REPEAT
1853	1d9s	A	608	743	9e-37	0.36	1.00	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1d9s	A	645	773	1.2e-34	0.43	1.00	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1d9s	A	677	807	3e-34	0.54	0.92	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1853	1dcq	A	513	694	4.5e-32	0.13	0.51	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1853	1fgk	A	18	293	1.5e-45		114.87	FGF RECEPTOR I; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1853	1fgk	A	26	276	1.5e-45	0.46	1.00	FGF RECEPTOR I; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1853	1fgk	B	1	292	7.5e-45		112.87	FGF RECEPTOR I; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF D score	SEQFOL D score	Compound	PDB annotation
1853	1fgk	B	26	276	7.5e-45	0.50	1.00	FGF RECEPTOR 1; CHAIN: A; B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1853	1fmk							TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1853	1fpu	A	49	276	7.5e-45	0.51	1.00	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A; B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1853	1hcl		19	326	9e-28			HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1853	1ihb	A	484	608	3e-34	0.36	1.00	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; B;	CELL CYCLE INHIBITOR P18-INK4C(INK6), CELL CYCLE INHIBITOR P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1853	1ikn	D	458	647	4.5e-46	0.41	1.00	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1ikn	D	486	680	6e-53	0.41	1.00	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1853	1ikn	D	551	749	6e-58	0.21	1.00	B-ALPHA; CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1ikn	D	584	775	4.5e-52	0.26	1.00	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1ikn	D	617	810	1.3e-54	0.15	1.00	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1853	1lr3	A	10	306	1.5e-46			INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1853	1lr3	A	26	276	1.5e-46	0.65	1.00	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1853	1myo							MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION NMR, ANK-REPEAT
1853	1myo							MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	SEQFOIL D score	Compound	PDB annotation
1853	1myo	461	589	8e-16	-0.06	0.46		MYOTROPHIN; CHAIN: NULL	ACETYLATION, NMR, ANK-REPEAT
1853	1myo	521	635	4.5e-32	0.55	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo	554	669	1.5e-36	0.44	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo	621	735	1.5e-32	0.34	0.99		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo	654	768	3e-33	-0.03	0.57		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo	684	800	1.5e-30	0.37	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1nf1	E	461	637	6e-43	0.50	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1nf1	E	484	677	3e-50	0.52	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1nf1	E	549	749	1.2e-53	0.54	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1nf1	E	581	778	1.5e-53	0.20	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1nf1	E	616	815	1.5e-53	0.56	1.00	NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E; F;	REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1853	1p38	4	359	3e-27			92.67	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1853	1pme	15	358	6e-29			97.49	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1853	1qcf	A	26	276	1.5e-49	0.66	1.00	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1853	1qpc	A	26	276	7.5e-50	0.71	1.00	LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA/BETA FOLD
1853	1sw6	A	466	592	1.5e-17	-0.40	0.10	REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1853	1sw6	A	512	759	1.5e-40	-0.17	0.00	REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1853	1yec	B	452	503	3.2e-12	0.27	0.96	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	1yec	B	458	578	6.4e-12	0.31	1.00	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
									P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	lycs	B	488	660	6e-33	0.09	0.99	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	lycs	B	554	726	1.4e-38	0.26	0.99	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1853	lycs	B	654	809	7.5e-33	-0.13	0.30	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFFOL D score	Compound	PDB annotation
1853	3erk		5	356	9e-31			107.86	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1854	1c1y	A	1	171	9.6e-68			85.26	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKogene SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1854	1ctq	A	1	173	9.6e-68	0.43	1.00		RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKogene SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1854	1ctq	A	1	173	1.6e-68	0.55	1.00		TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1854	1ctq	A	1	174	1.6e-68			77.02	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1854	1d5c	A	3	171	6.4e-56	0.48	1.00		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS, SECRETOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
1854	1ds6	A	1	176	3.2e-53	0.12	0.59		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SAND WHICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
1854	1ek0	A	1	174	6.4e-55	0.31	1.00		GTP-BINDING PROTEIN YPT51; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT1/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE
1854	1kao		1	171	4.8e-64	0.49	1.00		RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1854	1kao	1	174	4.8e-64			95.27		RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1854	1mh1	1	174	1.1e-53			52.65		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPase, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1854	1mh1	2	176	1.1e-53	0.28	0.94			RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPase, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1854	1pj1	1	171	4.8e-52	0.37	1.00			ONCOGENE PROTEIN C-H-RAS P21 PROTEIN MUTANT WITH GLY 12 REPLACED BY PRO	
									IPLJ 3 (G12P) COMPLEXED WITH P3-I-2.	
									NITROPHENYLETHYL- 1PLJ 4 GUANOSINE-5'-B(G-IMIDO)-TRIPHOSPHATE 1PLJ 5	
1854	1rrp	C	2	186	4.8e-36		50.36		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1854	1zbd	A	1	179	8e-59		60.15		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1854	1zbd	A	4	176	8e-59	0.43	0.96	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	BINDING/EFFECTOR, G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1854	2ngr	A	1	193	3.2e-50				BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A, COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1854	3rab	A	2	174	1.1e-59		54.33	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1854	3rab	A	4	174	1.1e-59		68.59	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1854	1fle	1	29	72	3.2e-16	-0.71	0.48	ELASTASE; CHAIN: E; ELAFIN; CHAIN: I;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1856	1fle	1							COMPLEX (SERINE PROTEASE/INHIBITOR) SKIN. DERIVED ANTI-EUKAROZOTENASE (SKALP); HYDROLASE, SERINE PROTEASE, 3D-STRUCTURE, ZYMOGEN, PANCREAS, 2 SIGNAL, COMPLEX (SERINE PROTEASE/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB ID
1856	1igf	A	32	80	0.0011	-0.54	0.12	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1856	2rel		20	72	1.6e-17	-0.02	0.46	R-ELAFIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R-ELAFIN, ELASTASE INHIBITOR
1857	1cly	A	19	177	9.6e-25		50.43	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKogene SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1857	1cz2	A	23	185	1.6e-28	-0.14	0.01	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTI PARALLEL COILED-COIL
1857	1d5c	A	21	183	3.2e-30	-0.22	0.01	RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
1857	1e0s	A	14	191	4.8e-52	0.11	1.00	ADP-RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
1857	1ek0	A	22	183	3.2e-28	0.06	-0.13	GTP-BINDING PROTEIN YPT31; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2, PROTEIN, ENDOCYTOSIS, HYDROLASE
1857	1fqq	A	7	190	1.1e-48	0.50	1.00	ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
1857	1hur	A	6	182	6.4e-57		83.99	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
1857	1hur	A	6	192	6.4e-57	0.23	0.92	HUMAN ADP-RIBOSYLATION	PROTEIN TRANSPORT GDP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMR score	SEQROL D score	Compound	PDB annotation
1857	1kao	19	186	1.6e-24					FACTOR 1; IHUR 5 CHAIN: A; B; IHUR 7 RAP2A; CHAIN: NULL;	BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16 GTP-BINDING PROTEIN GTP. BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)
1857	1lx4	B	23	185	1.6e-27	0.22	-0.03		P50 RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	GTPase-activating protein RHOGAP; complex (GTPase activation/proto-oncogene), GTPase, 2,1 transition state, GAP
1857	3rab	A	22	190	3.2e-33	-0.03	0.30		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1858	1alh	A	52	132	3.2e-30	-0.07	0.28		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1858	1alh	A	76	162	3.2e-31			58.29	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1858	1alh	A	80	160	3.2e-31	0.40	0.51		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, PROTEIN-DNA PROTEIN
1858	1mey	C	107	188	3.2e-50	-0.22	0.09		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
1858	1mey	C	51	132	4.8e-50	-0.18	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1858	1mey	C	79	160	1.4e-50	0.17	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1858	1mey	C	79	161	1.4e-50		62.32		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1858	1tf3	A	80	160	3.2e-20	0.14	0.24		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TEI1A; 5S GENE; NMR, TEI1A, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 TRANSCRIPTION REGULATION/DNA
1858	1ubd	C	56	160	1.3e-34	-0.08	0.39		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION REGULATION/DNA
1858	2gli	A	11	162	3.2e-33	-0.10	0.10		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
1858	2gli	A	51	188	4.8e-34		58.21	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1858	2gli	A	59	188	4.8e-34	-0.37	0.11	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1859	1alh	A	115	198	6.4e-29		60.10	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	117	197	6.4e-29	-0.04	0.78	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	145	237	4.8e-27	-0.23	0.35	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	212	273	6.4e-15	0.07	-0.13	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1alh	A	96	169	3.2e-25	-0.26	0.10	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	1mey	C	116	197	1.6e-50	-0.03	1.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1859	1mey	C	116	198	1.6e-50					(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	144	237	1.3e-46	-0.02	0.43		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	172	265	1.1e-33	-0.35	0.12		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	85	141	1.4e-26	-0.22	0.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	C	88	169	1.1e-41	-0.10	0.35		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1mey	G	209	237	1.4e-11	-0.11	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1859	1paa		212	239	8e-06	-0.29	0.81		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDUES 130 -	

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast	Verify score	PMIF score	SEQROL D score	Compound	PDB annotation
									159) 1PAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 1PAA 5 REPLACED BY ALA (P131A,P133A,C140A) (NMR, 10 STRUCTURES) 1PAA 6	
1859	1sp2								SPI2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI1
1859	1t3	A	105	169	1.1e-16	-0.52	0.00		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION(DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION(DNA)
1859	1t3	A	114	201	1.4e-20			55.20	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION(DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION(DNA)
1859	1t3	A	117	198	1.4e-20	-0.08	0.48		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION(DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQRFOL D score	Compound	PDB annotation
1859	1tf6	A	105	259	1.4e-28	-0.24	0.10		TFIIL _A ; CHAIN: A; D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION(DNA) COMPLEX (TRANSCRIPTION TRANSCRIPTION) (REGULATION(DNA) COMPLEX (TRANSCRIPTION TRANSCRIPTION) REGULATION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1tf6	A	117	275	1.1e-28	-0.01	0.33		TFIIL _A ; CHAIN: A; D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA) COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1tf6	A	50	237	1.1e-28			66.86	TFIIL _A ; CHAIN: A; D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA) COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1tf6	A	86	178	3.2e-16	-0.25	0.01		TFIIL _A ; CHAIN: A; D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA) COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1859	1ubd	C	110	220	3e-22	-0.00	0.45		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION TRANSCRIPTION(DNA) YTNG-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN

SEQ NO:	PDB ID	CHAI NID	STAR END AA	Psi Blast TAA	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
1859	lubd	C	152	265	3.2e-22	-0.06	0.07	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1859	lubd	C	86	198	3.2e-33		68.47	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1859	lubd	C	93	197	3.2e-33	-0.27	0.98	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1859	2adr		117	171	3.2e-16	-0.05	0.37	ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1859	2gli	A	106	199	6.4e-33	-0.22	0.33	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1859	2gli	A	83	238	6.4e-33		68.84	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1859	2gli	A	96	237	1.3e-31	0.04	0.04	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1860	1alh	A	371	452	4.8e-32	0.37	1.00	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1860	1alh	A	372	453	4.8e-32		69.01	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1860	1alh	A	399	488	3.2e-28	-0.35	0.41	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1860	1buo	A	4	126	1.3e-37	0.40	1.00	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1860	1buo	A	5	126	1.3e-37		64.40	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF D score	SEQFOL	Compound	PDB annotation
1860	1mey	C	336	423	1.6e-47	-0.44	0.09	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1mey	C	370	452	1.3e-50	0.14	1.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1mey	C	370	452	1.3e-50		67.59	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1mey	C	398	488	3.2e-47	-0.16	0.71	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	1tf3	A	399	488	3.2e-19	-0.48	0.23	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1860	1tf6	A	371	490	1.6e-31	-0.38	0.11	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

SEQ ID NO.	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1860	1ubd	C	344	448	1.1e-32	-0.05	0.92	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		COMPLEX (TRANSCRIPTION) REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1860	1ubd	C	375	488	6.4e-34	-0.03	0.89	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		COMPLEX (TRANSCRIPTION) REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION/DNA)
1860	1ubd	C	406	493	4.8e-24	-0.08	0.10	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		COMPLEX (TRANSCRIPTION) REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION/DNA)
1860	2gii	A	224	313	1.6e-09	0.05	-0.20	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1860	2gii	A	319	452	6.4e-34	0.10	0.07	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1860	2gli	A	344	490	1.6e-34	-0.09	0.11		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D; GLI1,ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	ZINC FINGER PROTEIN GLI1; COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI1,ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1861	1c40	A	470	630	1.6e-13	0.13	0.18		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERMETHYLATION-RESISTANT PROTEIN
1861	1d2m	A	470	630	1.6e-13	0.05	0.46		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A; EXCINUCLEASE ABC SUBUNIT B; CHAIN: A; EXCINUCLEASE UVRB COMPONENT UVRB; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1861	1d2m	A	538	662	1.4e-07	-0.11	0.39			HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1861	1d9x	A	457	658	6.4e-17	-0.27	0.24			GENE REGULATION APO PROTEIN
1861	1fuk	A	508	670	9.6e-39	0.23	0.55		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1861	1fuu	A	105	321	4.8e-43	0.09	-0.14		YEAST INITIATION FACTOR 4A; CHAIN: A; B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1861	1fuu	B	313	670	3.2e-91	0.06	0.43		YEAST INITIATION FACTOR 4A; CHAIN: A; B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1862	1byu	A	14	211	7.5e-64	0.35	1.00		GTP-BINDING PROTEIN RAN; CHAIN: A; B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1862	1byu	A	15	217	7.5e-64		113.24		GTP-BINDING PROTEIN RAN; CHAIN: A; B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1862	1byu	B	9	211	1.3e-65	0.44	1.00		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1862	1byu	B	9	215	1.3e-65			109.68	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1862	1cly	A	16	181	8e-65	0.51	1.00		RAS RELATED PROTEIN RAP-IA; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1862	1cly	A	17	181	8e-65			102.67	RAS RELATED PROTEIN RAP-IA; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1862	1ctq	A	17	182	6.4e-64	0.65	1.00		TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1862	1ctq	A	17	182	6.4e-64					SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1862	1cxz	A	19	182	3.2e-58			98.76	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1862	1d5c	A	18	179	3.2e-62	0.56	1.00		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKC; CHAIN: B; RAB6 GTPASE; CHAIN: A;	SIGNALING PROTEIN PROTEIN COMPLEX, ANTI PARALLEL COILED-COIL
1862	1ek0	A	18	179	9.6e-60	0.68	1.00		GTP-BINDING PROTEIN YPT51; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS,

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1862	1ibr	A	17	187	3e-60			113.50	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	HYDROLASE
1862	1ibr	A	18	186	3e-60	0.80	1.00		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1862	1kao		17	182	9.6e-59			98.96	RAP2A; CHAIN: NULL;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1862	1rrp	C	15	198	1.4e-60			114.45	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1862	1rrp	C	16	193	1.4e-60	0.45	1.00		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE) (NUCLEAR PROTEIN)
1862	1tx4	B	19	180	4.8e-55			87.88	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX (SMALL GTPASE) (NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1862	1zbd	A •	12	187	4.8e-69			130.15	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	ACTIVATIN/PROTO-ONCOGENE, ACTIVATION PROTEIN, GTPase, 2 TRANSITION STATE, GAP COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1862	1zbd	A	14	185	4.8e-69	0.65	1.00		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RAB3A, RABPHILIN COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1862	3rab	A	13	182	8e-70	0.78	1.00		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1862	3rab	A	13	182	8e-70			145.01	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1864	1a9n	B	135	202	7.5e-07	0.40	0.52		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1864	1b7f	A	138	207	3e-07	0.08	0.43		SXL-ELETAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*U)-CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA- PRE-MRNA, SPlicing REGULATION, RNP DOMAIN, RNA COMPLEX
1864	1cvj	A	138	205	7.5e-07	0.47	0.57		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1864	1cvj	F	136	199	7.5e-07	0.54	0.43		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)

SEQ ID NO.	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
									PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5' R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*)3'); CHAIN: M, N, O, P, Q, R, S, T;	BINDING PROTEIN I; PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1864	1fj7	A	136	196	6e-07	0.48	0.21		NUCLEOLIN RBD1; CHAIN: A; STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	
1864	1nrc	B	135	195	1e-08	0.13	0.99		RIBONUCLEOPROTEIN PROTEIN FROM U1 SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U1) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	
1864	1qm9	A	88	196	6e-07	0.20	0.15		POLYPYRIDINE TRACT-BINDING PROTEIN; CHAIN: A; TRANSLATION	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIDINE TRACT BINDING PROTEIN, RNP, RNA, SPlicing, 2
1864	2ula		136	195	6e-07	0.05	0.43		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEAR PROTEIN U1 SNRNP A; PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN
1864	2up1	A	138	196	7.5e-07	0.32	0.95		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1864	3sx1	A	138	207	3e-07	0.38	0.48		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
		*							SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSEAGE COMPENSATION
1865	1ses	A	439	542	3.2e-05	-0.21	0.01	LIGASE(SYNTETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	
1867	1xbt	A	1	94	1.6e-21	-0.88	0.60	T PROTEIN; CHAIN: A; B; DNA; CHAIN: C; D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN
1867	1xbtr	A	1	96	1.2e-37	-0.90	0.47	T PROTEIN; CHAIN: A; B; DNA; CHAIN: C; D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN
1870	1a4y	A	183	350	8e-08	0.30	0.43	RIBONUCLEASE INHIBITOR; CHAIN: A; D; ANGIOGENIN; CHAIN: B; E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULARrecognition, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1870	1a4y	A	209	338	1.4e-08	0.15	0.60	RIBONUCLEASE INHIBITOR; CHAIN: A; D; ANGIOGENIN; CHAIN: B; E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULARrecognition, EPITOPE MAPPING, LEUCINE-RICH

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1870	1a4y	A	209	373	3e-06	0.14	0.25		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1870	1d0b	A	196	333	8e-07	0.40	0.12		INTERNALIN B; CHAIN: A; INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1870	1f0l	A	222	354	0.00096	-0.10	0.25		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1870	1f0l	B	193	306	1.1e-06	0.03	0.03		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1870	1f0l								NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1870	1fqv	A	128	349	1.1e-46	0.45	0.51		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1870	1fs2	A	128	349	4.8e-36	0.22	0.72		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1870	1yrg	A	248	347	0.00064	0.09	0.27		GTPASE ACTIVATING	TRANSCRIPTION RNA IP, RANGAF;

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE score	Compound	PDB annotation
									PROTEIN RNA1_SCHPO; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1870	2bnh								RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1871	1bak		168	291	4.8e-10	0.08	-0.03		G-PROTEIN COUPLED RECEPTOR KINASE 2; CHAIN: NULL;	TRANSFERASE GRK-2, BETA-ADRENERGIC RECEPTOR KINASE 1, BETA-ARK PLECKSTRIN HOMOLOGY DOMAIN, PH DOMAIN, SIGNAL TRANSDUCTION, 2 G-BETA-GAMMA BINDING DOMAIN, BETA-ADRENERGIC RECEPTOR 3 KINASE, BETA-ARK, G-PROTEIN COUPLED RECEPTOR KINASE (GRK-2)
1871	1btn								BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
1871	1dro		182	264	1.5e-05	0.22	0.21		BETA-SPECTRIN; 1DRO 6 CHAIN: NULL; 1DRO 7	CYTOSKELETON
1871	1dyn	A	186	271	4.8e-10	0.13	0.11		SIGNAL TRANSDUCTION PROTEIN DYNAMIN (PLECKSTRIN HOMOLOGY DOMAIN)(DYNPH) 1DYN 3	
1871	1ef1	A	149	464	1.6e-58	0.05	0.53		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL STRUCTURE

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1871	1fao	A	170	269	3.2e-17	0.31	0.80	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHSN, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1871	1fb8	A	170	269	3.2e-17	0.14	0.69	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHSN, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1871	1fgy	A	172	272	4.8e-18	0.49	0.65	GPP; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
1871	1gc7	A	134	464	3.2e-58	-0.01	0.01	RADIXIN; CHAIN: A;	CELL ADHESION 3 SUBDOMAINS, CYTOSKELETON, CELL ADHESION
1871	1ps		169	285	1.4e-14	0.14	0.09	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (NSGIGI05-LEHHHHHH) (NMR, 25 STRUCTURES) 1PLS 5	
1872	1a05	A	5	390	0		69.11	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS
1872	1a05	A	8	387	0	0.03	0.54	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation	
								B;	DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS	
1872	1ai2	5	387	0	0.01	0.60		ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE OXALOSUCCINATE DECARBOXYLASE, IDH; OXIDOREDUCTASE (NAD(A)-CHOH(D)), NADP, PHOSPHORYLATION, 2 GLYOXYLATE BYPASS	
1872	1ai2	7	387	0			62.58	ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE OXALOSUCCINATE DECARBOXYLASE, IDH; OXIDOREDUCTASE (NAD(A)-CHOH(D)), NADP, PHOSPHORYLATION, 2 GLYOXYLATE BYPASS	
1872	1cm7	A	1	382	0			63.70	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, NAD-DEPENDANT ENZYME, 2 LEUCINE BIOSYNTHETIC PATHWAY
1872	1cm7	A	1	389	0	0.04	0.41	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, NAD-DEPENDANT ENZYME, 2 LEUCINE BIOSYNTHETIC PATHWAY	
1872	1cnz	A	1	382	0		60.42	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD-DEPENDANT ENZYME	
1872	1cnz	A	1	389	0	-0.04	0.65	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,	

SEQ ID NO:	PDB ID	CHAIN NID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
									B;	DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD-DEPENDANT ENZYME
1872	1idm		42	366	4.8e-95			54.18	3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	OXIDOREDUCTASE; 1IDM 7 CHIMERA 1IDM 20
1872	1idm	9	387	4.8e-95	0.06	0.42			3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	OXIDOREDUCTASE IPMDH; 1IDM 7 CHIMERA 1IDM 20
1872	1xac		42	366	1.6e-96			50.68	3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; 1XAC 8 CHAIN: NULL; 1XAC 9	OXIDOREDUCTASE IPMDH; IMDH; IXAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21
1872	1xac	9	387	1.6e-96	0.04	0.46			3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; 1XAC 8 CHAIN: NULL; 1XAC 9	OXIDOREDUCTASE IPMDH; IMDH; IXAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21
1872	2ayq	A	6	387	0	-0.03	0.57		3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A; B;	OXIDOREDUCTASE 3-ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE
1872	2ayq	A	6	388	0			68.62	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A; B;	OXIDOREDUCTASE 3-ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE
1873	1a5e		10	125	1.6e-23	0.44	0.51		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1873	1awc	B	10	156	4.8e-36	0.11	0.22		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION
1873	1awc	B	2	125	6.4e-33	0.43	1.00		GA BINDING PROTEIN ALPHA, CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1873	1bd8								GA BINDING PROTEIN ALPHA, CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1873	1bd8		3	128	1.1e-23	0.22	0.96		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1873	1bi7	B	10	125	8e-24	0.52	0.62		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1873	1bx	B	13	157	8e-33	0.18	0.15		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR, CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMR score	SEQFOL D score	Compound	PDB annotation
1873	1bix	B	3	128	1.6e-22	0.42	0.96		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1873	1bu9	A	10	153	6.4e-34	0.16	0.71		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR.
1873	1bu9	A	2	130	4.8e-27	0.15	0.55		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR.
1873	1d9s	A	10	131	3.2e-24	0.05	0.49		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1873	1ihb	A	10	153	6.4e-34	0.23	0.60		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1873	1ihb	A	2	129	1.6e-26	0.14	0.74		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1873	1myo		11	127	1.3e-24	0.21	0.64		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN ACETYLATION, NMR, ANK-REPEAT
1873	1nfi	E	4	212	3.2e-40	0.02	0.45		NE-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B PSO; CHAIN: B, D;	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
									I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1874	1a5e		10	120	3.2e-16	0.03	0.81		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1874	1bd8		13	153	3.2e-27	0.03	0.31		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1874	1bd8		2	120	1.4e-15	-0.04	0.01		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1874	1bi7	B	10	120	3.2e-17	0.18	0.68		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1874	1bi7	B	52	153	1.4e-17	0.15	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1874	1bix	B	13	153	3.2e-25	0.09	0.31		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	SEQFOL D score	Compound	PDB annotation
1874	1blx	B	2	120	1.6e-14	0.08	-0.09	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1874	1bu9	A	13	158	1.3e-29	-0.15	0.23	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1874	1bu9	A	2	125	1.3e-18	0.04	0.11	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1874	1bu9	A	54	212	6.4e-28	0.01	0.05	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1874	1d9s	A	10	120	1.6e-17	0.28	0.33	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1874	1dcq	A	13	122	1.5e-12	0.08	0.69	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1874	1hb	A	2	124	4.8e-18	0.40	0.71	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1874	1lib	A	54	211	3.2e-27	-0.09	0.27		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; INHIBITOR	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 46-
1874	1myo	*	11	138	1.1e-21	-0.17	0.24		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT INHIBITOR
1874	1myo	73	159	1.1e-21	0.30	0.23		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	
1874	1ycs	B	60	193	4.8e-20	-0.03	0.01	P53; CHAIN: A; S3BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, 3 DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)	
1877	1alh	A	239	335	9.6e-26	0.12	0.66	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B; C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	
1877	1alh	A	243	336	7.5e-29	0.04	0.00	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B; C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	
1877	1alh	A	283	365	7.5e-29		72.03	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B; C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	
1877	1alh	A	395	502	1.5e-39	-0.14	0.09	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA),	

SEQ ID NO.	PDB ID	CHAI ND	STAR TAA	END AA	Psi Blast score	PMF D score	SEQFOL D score	Compound	PDB annotation
1877	1mey	C	161	263	4.8e-42	-0.16	0.06	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1877	1mey	C	166	307	1e-11	-0.57	0.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	190	335	3e-26	-0.46	0.37	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	217	307	8e-40	-0.24	0.07	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	266	335	1.3e-39	0.02	0.95	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	282	363	6.4e-50	0.29	1.00	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	282	364	8e-51		98.05	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	310	391	8e-51	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	338	419	3.2e-51	0.43	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	366	447	1.3e-50	0.28	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	394	473	4.8e-47	0.20	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	422	529	3e-40	-0.02	0.82		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	450	529	3.2e-48	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	C	476	533	8e-34	0.46	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
1877	1mey	G	187	214	1.6e-11	-0.12	0.48	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
1877	1mey	G	236	263	6.4e-12	-0.05	0.52	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
1877	1sp2	-	190	218	9.6e-07	0.02	0.09	SPIF2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI	
1877	1tf3	A	239	335	4.8e-17	0.27	0.07	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIA; 5S GENE; NMR, TFIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	
1877	1tf6	A	162	316	8e-31	-0.24	0.11	TFIIA; CHAIN: A; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION (REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	
1877	1tf6	A	239	400	9.6e-36	-0.06	0.75	TFIIA; CHAIN: A; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1877	1tf6	A	310	471	7.5e-68			CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1tf6	A	311	454	8e-38	-0.02	0.99	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1tf6	A	367	511	4.8e-38	0.12	1.00	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1tf6	A	395	531	8e-34	0.17	0.95	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	1ubd	C	165	335	1.4e-26	-0.39	0.37	YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
								ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	Iubd	C	243	363	7.5e-40	-0.00	0.98	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	Iubd	C	246	363	6.4e-33	-0.09	0.86	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	Iubd	C	287	391	3e-50	0.00	1.00	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	Iubd	C	318	419	3.2e-35	-0.13	0.95	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION(DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)
1877	Iubd	C	340	448	3e-48			86.32	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)
1877	Iubd	C	364	474	1.1e-47	0.26	0.99	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)	
1877	Iubd	C	374	473	4.8e-32	0.03	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION/DNA)
1877	Iubd	C	392	501	3e-48	0.10	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1877	1ubd	C	420	530	1.5e-48	0.12	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	C	430	529	8e-34	-0.03	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	2adr								ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1877	2adr								ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1877	2gli	A	190	365	1.5e-46	0.15	0.80		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gli	A	246	390	3.2e-33	0.19	0.41		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gli	A	282	421	1.5e-66			93.76	ZINC FINGER PROTEIN GLII;	COMPLEX (DNA-BINDING

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C; D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gli	A	310	503	1.5e-66	-0.16	0.27		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1877	2gli	A	395	533	6e-53	-0.16	0.93		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1878	1d2n	A	169	424	3.2e-15			65.03	N-ETHYLMALEIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1878	1d2n	A	196	349	3.2e-15	0.35	0.64		N-ETHYLMALEIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1878	1e94	E	169	270	3.2e-13	-0.74	0.10		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLU, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
1878	1fmn	A	184	405	1.5e-15	0.22	0.28		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDCC6; CDC6, CDCC18, ORC1, AAA-PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL
1878	1g41	A	169	360	1.6e-16	0.00	0.57		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1878	1g41	A	183	442	4.5e-34	0.16	0.23		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1878	2cmk	A	218	245	0.0045	-0.51	0.15		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1882	1ajs	A	54	499	1.6e-58		77.13	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE
1882	1ajs	A	89	517	1.6e-58	0.08	0.88	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE
1882	1ars		85	457	1.6e-64	-0.19	0.51	TRANSFERASE(AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1.) COMPLEXED WITH IARS 3 PYRIDOXAL-5'-PHOSPHATE IARS 4	
1882	1ars		95	508	1.6e-64		76.94	TRANSFERASE(AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1.) COMPLEXED WITH IARS 3 PYRIDOXAL-5'-PHOSPHATE IARS 4	
1882	1ax4	A	68	523	4.8e-13		71.45	TRYPTOPHANASE; CHAIN: A, B, C, D;	TRYPTOPHAN BIOSYNTHESIS; TRYPTOPHAN INDOLE-LYASE; TRYPTOPHAN BIOSYNTHESIS, TRYPTOPHAN INDOLE-LYASE, PYRIDOXAL 2' 5'-PHOSPHATE, MONOVALENT CATION BINDING SITE
1882	1b8g	A	80	515	0	0.44	1.00	1-AMINOCYCLOPROANE-1-CARBOXYLATE SYNTHASE; CHAIN: A, B;	LYASE ACC SYNTHASE, S-ADENOSYL-L-METHIONINE ETHYLENE BIOSYNTHESIS
1882	1b9h	A	181	304	1.6e-10	0.08	0.33	3-AMINO-5-	RIFAMYCIN BIOSYNTHESIS (RIFD)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation	
									HYDROXYBENZOIC ACID SYNTHASE; CHAIN: A;	GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)	
1882	1bjw	A	102	515	9.6e-84	0.52	1.00		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE, PYRIDOXAL ENZYME	
1882	1bjw	A	83	514	9.6e-84			134.98	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE, PYRIDOXAL ENZYME	
1882	1bw0	A	66	520	1.6e-67	0.24	1.00		TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, PYRIDOXAL 5'-PHOSPHATE, PLP	
1882	1bw0	A	92	520	1.6e-67			158.29	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, 2 AMINOTRANSFERASE, 2 PYRIDOXAL 5'-PHOSPHATE, PLP	
1882	1c7n	A	125	514	6e-52	0.34	1.00		CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE TRANSFERASE, PYRIDOXAL PHOSPHATE	
1882	1cs1	A	144	302	1.6e-08	-0.10	0.13		CYSTATHIONINE GAMMA-SYNTHASE; CHAIN: A, B, C, D;	LYASE CGS; LYASE, LIP-DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS	
1882	1d2f	A	128	514	4.5e-53	0.35	1.00		MALY PROTEIN; CHAIN: A, B;	TRANSFERASE	
									LARGE PLP-BINDING DOMAIN, SMALL C-2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE.	AMINOTRANSFERASE FOLD,	
1882	1dfo	A	182	415	4.8e-07	0.42	1.00	SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT, SERINE ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD	METHYLASE; ALPHA-PLP	
1882	1elj	A	123	514	9.6e-13	0.17	0.87		L-CYSTEINE/L-CYSTINE C-S LYASE; CHAIN: A, B;	LYASE FES CLUSTER	BIOSYNTHESIS, PYRIDOXAL 5'-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1882	1yaa	A	76	516	4.8e-52			79.51	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE ENZYME-PRODUCT COMPLEX
1882	1yaa	A	89	452	4.8e-52	0.06	1.00		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	AMINOTRANSFERASE
1882	2ayl	A	79	488	8e-53			74.67	AMINOTRANSFERASE; CHAIN: A, B, C, D; AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE
1882	2ayl	A	85	457	8e-53	-0.16	0.88		AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE
1882	2cst	A	81	517	1.6e-58	-0.13	0.95		AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AROAT; AMINOTRANSFERASE AROAT;
1882	2cst	A	38	499	1.6e-58			75.00	TRANSFERASE(AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5'-PHOSPHATE AND MALEATE 2CST 4	AMINOTRANSFERASE
1882	2ql	A	110	508	1.1e-48	0.01	0.34		TYROSINE PHENOL-LYASE; CHAIN: A, B;	LYASE LYASE, PLP-DEPENDENT ENZYME, PYRIDOXAL PHOSPHATE
1882	3tat	A	80	457	9.6e-58	-0.17	0.95		TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	AMINOTRANSFERASE PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC

SEQ ID NO:	PDB ID	CBM N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
1882	3rat	A	95	497	9.6e-58			91.42	TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	SUBSTRATES, PLP ENZYME AMINOTRANSFERASE; PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC SUBSTRATES, PLP ENZYME
1882	7aat	A	73	457	6.4e-65	-0.10	0.43		TRANSFERASE(AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'-PHOSPHATE AT PH 7.5 7AAT 4	
1882	7aat	A	88	492	6.4e-65			78.03	TRANSFERASE(AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'-PHOSPHATE AT PH 7.5 7AAT 4	
1883	1lar	B	3	220	1.1e-58	-0.13	0.18		LAR; CHAIN: A, B;	HYDROLASE TYROSINE PHOSPHATEASE, LAR PROTEIN
1883	1mkp		52	200	6.4e-24			68.80	PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1883	1mkp		55	200	6.4e-24	0.57	1.00		PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1883	1yhr	A	37	208	7.5e-31			139.04	HUMAN VHI-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1883	1yhr	A	50	200	7.5e-31	0.74	1.00		HUMAN VHI-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1884	1ae6	H	20	242	9.6e-82	0.30	1.00		ANTIBODY CTM01; CHAIN: L,	IMMUNOGLOBULIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									H ₃	IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
1884	1afv	H	20	244	8e-84	0.43	1.00		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1884	1bd2	E	21	261	1.2e-81			301.81	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1884	1bd2	E	22	261	1.2e-81	0.66	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1884	1bec		21	261	1.5e-76			273.44	14.3-D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
1884	1d5i	H	20	244	1.3e-81	0.23	0.99		CHIMERIC GERMINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
1884	1e6o	H	20	244	4.8e-81	0.40	1.00		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA
1884	1fvd	B	20	247	1.1e-84	0.18	1.00		IMMUNOGLOBULIN FAB	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
									FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1884	1igc	H	20	247	1.6e-83	0.22	1.00		COMPLEX (ANTIBODY BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) STREPTOCOCCUS IIGC15	
1884	1igt	B	20	282	3.2e-90	-0.00	0.98		IGG2A INTACT ANTIBODY - MAE231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1884	1igy	B	21	282	3.2e-82	0.07	0.82		IGG1 INTACT ANTIBODY MAE61.1;3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION, C REGION, Hinge REGION
1884	1ngp	H	20	244	1.6e-83	0.21	1.00		NIg9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN, IMMUNOGLOBULIN VARIABLE
1884	1nqb	A	12	130	9e-07	0.22	1.00		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
1884	1tcr	B	19	262	8e-71			277.99	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR: T-CELL, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1885	1g41	A	314	369	0.0094	-0.34	0.04		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1886	1buo	A	10	129	4.8e-24	0.34	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	PsiBlast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									AP*AP*AP*A)-3'; CHAIN: M, N, O, P, Q, R, S, T;
1887	1d8z	A	1342	1410	4.5e-05	0.45	1.00	HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1887	1fjc	A	1331	1417	3e-05	0.42	0.65	NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RNA-BINDING DOMAIN, NUCLEOLUS
1887	1osm	A	14	207	4.5e-09	0.70	-0.20	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1887	1pho		11	218	7.5e-10	0.77	-0.19	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	
1887	1qq4	A	37	204	4.5e-08	0.89	-0.19	ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1887	1sxl		1325	1396	0.00015	0.07	0.54	RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 -294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
1887	2sxl		1339	1410	0.00015	0.47	1.00	SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1887	2u2f	A	1342	1410	1.3e-05	0.44	0.99	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPlicing, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1887	3sxd	A	1339	1432	6e-05	0.01	0.55	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA-BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1888	1sx1								CHAIN: A;	BARREL, BACTERIAL SERINE PROTEASE
1888	1sx1		1286	1357	0.00015	0.07	0.54		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN) ISXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
1888	2sx1		1300	1371	0.00015	0.47	1.00		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1888	2uf2	A	1303	1371	1.3e-05	0.44	0.99		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN U2 SNRNP, RBD, RNA-BINDING PROTEIN
1888	3sx1	A	1300	1393	6e-05	0.01	0.55		SEX-LETHAL; CHAIN: A, B, C;	BINDING DOMAIN RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR,
1889	1b7f	A								TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1889	1cvj	A								
1889	1b7f	A	1245	1313	9e-05	0.53	1.00		SEX-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING
1889	1cvj	A	1245	1313	3e-05	0.41	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*3'); CHAIN: P, Q; O, P, Q, R, S, T;	REGULATION, RNP DOMAIN, RNA COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1889	1cvj	B	1243	1313	3e-05	0.41	0.89	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*3') CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1; PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1889	1d8z	A	1245	1313	4.5e-05	0.45	1.00	HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1889	1fjc	A	1234	1320	3e-05	0.42	0.65	NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1889	1asm	A	14	207	4.5e-09	0.70	-0.20	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1889	1pho		11	218	7.5e-10	0.77	-0.19	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHO) IPHO 3	
1889	1qq4	A	37	204	4.5e-08	0.89	-0.19	ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1889	1sxl		1228	1299	0.00015	0.07	0.54	RNA-BINDING PROTEIN SEX-LETHAL PROTEIN; CHAIN: 5	
1889	2sxl	*	1242	1313	0.00015	0.47	1.00	SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPlicing
1889	2u2f	A	1245	1313	1.3e-05	0.44	0.99	SPlicing FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPlicing, U2 SNRNP, RBD, RNA-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1889	3ssx	A	1242	1335	6e-05	0.01	0.55		SEX-LETHAL; CHAIN: A, B, C;	PROTEIN RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1894	1bj8									
1894	1bpv		166	262	1.6e-12	0.21	0.23		GPI30; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1894	1bpv		165	265	9.6e-11	0.07	0.70		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1894	1cfb		165	266	1.2e-12	0.18	0.94		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1894	1fjh	A	162	355	1.6e-16	0.02	-0.18		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1894	1qg3	A	168	450	6.4e-28			57.74	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1894			168	348	9.6e-17	0.28	-0.06		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	HEPARIN AND INTEGRIN BINDING STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1894	1qr4	A	164	261	4.5e-13	-0.24	0.29	TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1894	1qr4	A	169	349	9.6e-15	0.09	0.12	TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1894	1qr4	A	271	450	4.8e-15	0.03	-0.20	TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1894	1ttf		164	265	3e-13	0.15	0.49	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	
1895	1di2	A	230	293	1.1e-07	0.30	0.42	DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5'-R*GP*GP*CP*GP*CP*GP*CP*G P*CP*C)-3'; CHAIN: C, D, E, G; RNA BINDING PROTEIN; RNA BINDING PROTEIN/RNA	RNA BINDING PROTEIN/RNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINING PROTEIN, RNA BINDING PROTEIN/RNA
1895	1e0m	A	20	49	0.0003	-0.10	0.41	WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1895	1ekz	A	226	293	6e-12	0.57	0.70	MATERNAL EFFECT PROTEIN (STAUFFEN); CHAIN: A; STAUFFEN DOUBLE-STRANDED RNA BINDING DOMAIN; CHAIN: B;	CELL CYCLE RNA DSRBDII; NMR STRUCTURE, PROTEIN/RNA, PROTEIN DSRBD, DROSOPHILA, RNA 2 HAIRPIN
1895	1f8a	B	11	49	0.0006	-0.46	0.29	PEPTIDYL-PROLYL CIS-TRANS	ISOMERASE PIN1; PEPTIDYL-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ISOMERASE NIMA-CHAIN B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
1895	1stu		233	293	3e-05	0.13	0.25		MATERNAL EFFECT PROTEIN STAUFEN; 1STU 4	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13

TABLE 6

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
949	24	0.926	0.738
950	24	0.976	0.913
951	22	0.982	0.872
952	41	0.937	0.604
953	23	0.896	0.747
954	16	0.945	0.737
955	45	0.964	0.657
956	48	0.994	0.855
957	31	0.984	0.921
958	23	0.966	0.812
959	36	0.994	0.757
960	20	0.977	0.902
961	18	0.968	0.799
962	24	0.882	0.599
963	34	0.921	0.652
964	25	0.921	0.787
965	33	0.967	0.803
966	30	0.978	0.786
967	28	0.980	0.893
968	24	0.976	0.913
969	22	0.984	0.928
970	26	0.949	0.664
971	23	0.996	0.936
972	28	0.929	0.700
973	26	0.976	0.875
974	17	0.919	0.828
975	28	0.976	0.653
976	30	0.996	0.894
977	17	0.953	0.784
978	22	0.982	0.872
979	19	0.890	0.552
980	18	0.984	0.958
981	19	0.981	0.916
982	19	0.995	0.971
983	21	0.980	0.904
984	21	0.980	0.904
985	16	0.961	0.916
986	26	0.951	0.801
987	43	0.992	0.943
988	41	0.937	0.604
989	43	0.994	0.659
990	29	0.986	0.848
991	37	0.984	0.878
992	19	0.942	0.693
993	22	0.982	0.872
995	19	0.993	0.931
996	22	0.992	0.807
997	28	0.990	0.919
998	23	0.896	0.747
999	23	0.985	0.951
1000	21	0.989	0.925
1001	11	0.900	0.758
1002	18	0.933	0.634
1004	16	0.881	0.607

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1005	18	0.964	0.812
1006	19	0.972	0.915
1007	24	0.997	0.929
1008	16	0.945	0.737
1009	31	0.957	0.775
1010	22	0.975	0.822
1011	28	0.946	0.799
1012	24	0.973	0.910
1013	29	0.968	0.769
1014	25	0.977	0.776
1015	41	0.986	0.847
1016	28	0.988	0.938
1017	23	0.976	0.897
1018	45	0.964	0.657
1019	28	0.956	0.604
1020	33	0.948	0.776
1021	18	0.930	0.679
1022	26	0.947	0.594
1023	31	0.991	0.925
1024	41	0.942	0.703
1025	36	0.910	0.749
1026	24	0.988	0.919
1027	27	0.962	0.696
1028	23	0.965	0.693
1029	22	0.962	0.919
1030	24	0.943	0.832
1031	34	0.973	0.817
1032	22	0.947	0.677
1033	25	0.889	0.718
1034	27	0.962	0.856
1035	19	0.967	0.909
1036	39	0.986	0.922
1037	28	0.982	0.924
1038	44	0.974	0.662
1039	29	0.984	0.763
1040	22	0.974	0.796
1041	29	0.928	0.725
1051	23	0.966	0.812
1054	19	0.951	0.895
1055	16	0.927	0.827
1056	25	0.949	0.823
1058	28	0.980	0.848
1061	24	0.965	0.891
1062	25	0.946	0.860
1067	36	0.964	0.648
1074	32	0.941	0.669
1076	17	0.995	0.974
1083	18	0.968	0.799
1089	24	0.882	0.599
1091	38	0.991	0.904
1094	29	0.963	0.888
1096	19	0.892	0.715
1101	34	0.921	0.652
1102	20	0.951	0.839
1106	31	0.921	0.659
1110	36	0.992	0.917

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1124	30	0.989	0.910
1125	28	0.974	0.851
1127	25	0.937	0.812
1130	30	0.978	0.786
1131	27	0.987	0.879
1133	23	0.923	0.655
1144	28	0.980	0.893
1147	27	0.963	0.833
1150	24	0.976	0.913
1151	24	0.988	0.967
1152	22	0.968	0.831
1154	21	0.952	0.822
1155	42	0.939	0.682
1157	22	0.984	0.928
1158	22	0.984	0.928
1165	21	0.942	0.713
1167	18	0.922	0.838
1170	18	0.988	0.944
1174	18	0.975	0.958
1175	18	0.975	0.958
1176	18	0.975	0.958
1177	48	0.989	0.889
1178	23	0.996	0.936
1180	16	0.967	0.933
1193	15	0.948	0.907
1195	27	0.936	0.689
1196	42	0.978	0.750
1197	15	0.977	0.966
1199	26	0.976	0.875
1200	28	0.973	0.822
1201	28	0.990	0.925
1205	22	0.982	0.933
1206	15	0.986	0.919
1207	27	0.994	0.900
1215	21	0.989	0.871
1220	28	0.976	0.653
1226	20	0.987	0.916
1229	30	0.996	0.894
1230	41	0.983	0.791
1234	20	0.978	0.893
1239	17	0.953	0.784
1240	25	0.950	0.897
1241	20	0.974	0.912
1242	15	0.974	0.817
1247	35	0.973	0.795
1250	22	0.982	0.872
1251	18	0.983	0.927
1254	20	0.934	0.828
1255	16	0.952	0.807
1256	19	0.904	0.656
1260	35	0.957	0.640
1261	35	0.957	0.640
1263	33	0.953	0.707
1264	24	0.981	0.884
1265	24	0.987	0.914
1266	21	0.977	0.905

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1267	24	0.978	0.911
1268	18	0.984	0.958
1269	18	0.984	0.958
1270	24	0.989	0.922
1271	18	0.984	0.956
1272	18	0.986	0.965
1273	18	0.986	0.965
1276	32	0.956	0.706
1277	48	0.983	0.616
1278	20	0.965	0.878
1282	16	0.921	0.828
1283	20	0.937	0.700
1293	19	0.995	0.971
1294	19	0.995	0.971
1296	20	0.926	0.751
1302	29	0.981	0.937
1310	27	0.977	0.849
1314	24	0.977	0.845
1315	23	0.990	0.833
1317	25	0.971	0.894
1318	16	0.961	0.916
1319	41	0.980	0.681
1328	17	0.977	0.921
1329	26	0.993	0.894
1331	25	0.986	0.939
1333	33	0.977	0.811
1340	43	0.992	0.943
1341	20	0.943	0.882
1343	20	0.995	0.933
1344	26	0.938	0.663
1346	21	0.955	0.767
1347	19	0.920	0.692
1348	41	0.937	0.604
1349	41	0.937	0.604
1353	19	0.986	0.961
1357	41	0.923	0.559
1359	25	0.973	0.853
1361	20	0.935	0.817
1364	29	0.958	0.637
1365	23	0.991	0.740
1368	29	0.986	0.848
1369	18	0.997	0.979
1373	16	0.979	0.964
1375	25	0.980	0.952
1376	37	0.989	0.822
1378	37	0.984	0.878
1379	42	0.978	0.698
1380	18	0.969	0.913
1383	31	0.981	0.856
1386	36	0.987	0.595
1387	27	0.955	0.786
1389	17	0.915	0.825
1390	34	0.954	0.783
1393	19	0.941	0.839
1396	27	0.944	0.778
1397	20	0.941	0.734

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1404	22	0.982	0.872
1427	19	0.993	0.931
1428	22	0.992	0.807
1430	22	0.918	0.716
1433	38	0.994	0.887
1436	24	0.914	0.588
1438	28	0.990	0.919
1442	26	0.990	0.969
1446	36	0.954	0.817
1450	23	0.896	0.747
1451	23	0.969	0.855
1456	24	0.985	0.932
1462	23	0.985	0.951
1464	27	0.985	0.927
1465	21	0.960	0.649
1467	41	0.990	0.922
1468	20	0.991	0.954
1469	20	0.991	0.954
1473	21	0.975	0.909
1478	11	0.900	0.758
1493	18	0.933	0.634
1495	22	0.899	0.639
1496	40	0.953	0.668
1509	16	0.881	0.607
1516	36	0.924	0.590
1517	25	0.919	0.718
1518	28	0.928	0.590
1519	27	0.967	0.872
1526	25	0.998	0.934
1527	30	0.973	0.829
1547	20	0.937	0.728
1551	30	0.962	0.801
1552	17	0.925	0.779
1557	20	0.981	0.910
1562	17	0.977	0.921
1565	25	0.938	0.677
1568	22	0.975	0.822
1577	34	0.934	0.552
1578	28	0.946	0.799
1583	15	0.954	0.725
1584	30	0.938	0.808
1592	24	0.973	0.910
1597	24	0.920	0.596
1600	29	0.968	0.769
1604	28	0.975	0.926
1613	25	0.977	0.776
1618	41	0.986	0.847
1627	24	0.915	0.578
1630	24	0.950	0.737
1631	28	0.987	0.785
1632	19	0.890	0.552
1633	22	0.968	0.934
1634	22	0.968	0.934
1635	23	0.965	0.883
1636	23	0.965	0.883
1638	26	0.896	0.615

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1641	30	0.956	0.665
1644	39	0.971	0.694
1646	44	0.992	0.576
1649	45	0.964	0.657
1650	45	0.964	0.657
1653	17	0.968	0.947
1655	28	0.960	0.607
1657	31	0.977	0.720
1662	28	0.956	0.604
1666	47	0.985	0.646
1667	19	0.990	0.946
1677	47	0.996	0.556
1684	18	0.930	0.679
1687	25	0.992	0.948
1689	26	0.947	0.594
1693	22	0.963	0.859
1695	26	0.956	0.830
1703	26	0.990	0.959
1706	40	0.987	0.917
1707	26	0.985	0.917
1710	36	0.991	0.868
1713	24	0.887	0.553
1714	23	0.995	0.974
1715	18	0.997	0.977
1716	22	0.968	0.934
1718	26	0.974	0.730
1721	18	0.983	0.939
1731	24	0.988	0.919
1743	30	0.939	0.639
1744	26	0.984	0.746
1755	23	0.965	0.693
1758	22	0.962	0.919
1759	21	0.988	0.911
1760	36	0.980	0.559
1769	10	0.880	0.780
1771	14	0.922	0.678
1773	39	0.982	0.829
1778	34	0.973	0.817
1779	36	0.976	0.794
1786	18	0.918	0.651
1787	35	0.991	0.834
1789	22	0.947	0.677
1795	24	0.963	0.865
1796	30	0.967	0.758
1797	33	0.926	0.807
1800	25	0.889	0.718
1805	20	0.995	0.968
1807	27	0.887	0.642
1810	41	0.975	0.875
1813	26	0.921	0.620
1826	36	0.951	0.782
1832	19	0.983	0.888
1833	23	0.971	0.941
1834	40	0.964	0.560
1839	39	0.942	0.587
1846	16	0.945	0.737

SEQ ID NO:	Position of Signal in Amino Acid Sequence	maxS (Maximum score)	meanS (Mean score)
1847	24	0.946	0.593
1848	44	0.974	0.662
1850	26	0.974	0.730
1851	27	0.952	0.832
1856	25	0.960	0.642
1866	31	0.956	0.846
1869	16	0.968	0.921
1884	19	0.984	0.936

TABLE 7

SEQ ID	Chromosomal location
1	X
2	Xp21.2-p11.2
3	2
4	2
5	8
6	8
7	17
10	17
13	9
14	Xq24-q25
15	Xq24-q25
16	9p21
17	16
19	7q32
20	2
21	2
22	11
23	12q
27	22q11
28	6p
29	6p23
31	17q
32	12
33	2p23.3-q34
34	9q31-q32
35	19
36	19
37	19q13.3
38	6p21.3
39	10q26.2-10q26.3
40	3
42	12
43	6p21-p12
44	13q12-13
46	2
47	3
48	15q15
49	22q13.33
50	5q14-q22
51	X
52	19cen-q13.2
53	3p26

SEQ ID	Chromosomal location
54	2p24.3
55	3p26
56	3p26
57	15
60	15
62	1p21.2-22.3
65	11q12-q13.1
66	xp11
67	20q11.21-q13.12
69	2
70	X
71	1
72	1q21.2-q21.3
73	17p11.2
74	X
75	19
76	9
80	19
83	6q16
85	15
86	12
87	17q22-q24
88	8q22-q23
90	15
91	14q32.3
94	14
95	7
96	10q26.1
97	9p21
98	16q24.3
99	5
101	15
102	19
103	6p21.3
104	11p15.3-p15.4
105	16
107	14q32.1-q32.2
111	11q13
112	9
114	2q35
115	22q13
116	16
117	16
118	16q24.3
120	19
122	1
123	20
124	9
125	3
126	11
127	22q11.2
128	20q11.2-12
129	14
131	10q25.1
133	17p11.2
134	20
136	4p16.3

SEQ ID	Chromosomal location
137	12p13
138	19
139	1p34.1-p32
140	4 or 17
143	Xq13.1-13.3
144	3
145	3
146	5
147	9
148	11q13
149	6
150	15
151	19
152	Xp11.21-11.23
153	18q22-q23
155	16
157	4
160	1p36.23-p33
161	9q22.2
163	4
165	3
166	17
167	6p21.3
168	16
169	9
170	19
171	15
172	2p25
173	22q11.21
174	18q22
179	6p21.3
180	15q14
181	5q
183	5
184	11
187	11
188	3p21.3
189	12p13-qter
190	12p13-qter
191	12p13-qter
192	12p13-qter
193	2q34-q35
194	2q34-q35
195	10
199	7q11-q22
200	7q22.1-7q31.33
201	3
202	19q13.4
203	3
205	Xq28
206	6
208	Xq26.2-27.2
209	4
210	4
211	1q31
212	19q12-19q13.1
213	6q23

SEQ ID	Chromosomal location
214	10
215	1
216	1p32.2-34.2
217	8
218	11q13
219	1q21-q23
220	Xq28
221	16
222	17
223	1
224	19p13.3
225	19p11-q11
226	1
227	1
228	1
229	12
230	5
231	1p31
232	1p31.1-p22.3
233	22q11.23
234	22q12.1-q12.3
235	1
236	17
237	15
238	2p13
239	17
241	11p13
242	11
243	4q22-q24
244	12
245	19
246	5
247	14
248	16
249	14
250	4
251	19
252	9p22-p21 or 9p13
256	11q
257	9q33-q34.1
258	12pter-p13.31
260	8
261	11q14
262	17
263	12q13
264	16q13-q21
265	16q13-q21
267	6q26-27
268	9q12-q21.2
269	9q12-q21.2
270	9q12-q21.2
271	19
272	1p34.1-35.3
273	11
274	11
275	X
277	2

SEQ ID	Chromosomal location
278	16
280	19q13.1-q13.2
282	12
284	2p23.3-q24.3
285	11p15
286	19
287	7
288	10
290	12
293	3q23-q24
294	1p34.1-35.3
295	p22.2-31.1
296	3q22-q24
297	6
299	2p11
300	16
301	10q24
302	10
304	12q22-q23
305	17pter-p11
307	1p35-p34
308	9
309	16
310	21
311	12p13
312	1
313	1
314	17
315	1q42-q43
316	6p21.32-22.1
317	6p21.32-22.1
318	6p21.32-22.1
319	6p21.32-22.1
320	6p21.32-22.1
321	6p21.32-22.1
322	6p21.32-22.1
323	6p21.32-22.1
324	6p21.32-22.1
325	6p21.32-22.1
326	17
327	3
328	14
332	17
335	17
336	14q32
337	8q23
338	8q23
339	16q11.1-q11.2
340	8q22-q23
341	16p13.3
342	18
343	15
344	17
345	20q11.2-q13.1
346	20q11.2-q13.1
347	19q13.3
348	19

SEQ ID	Chromosomal location
349	17q25.1
350	18
351	11
352	1
353	q25.1-31.1
354	11q14
355	1q31
356	1q31
357	18
358	3p
359	10
360	7q22
361	7q22
362	1q21.3
363	3
364	18q12
365	11p15
367	14
369	1p36.21
371	6p12.3-21.1
373	14q13.1-14q21.3
374	15
375	4
376	7q32-q34
377	7q32-q34
378	20q13.1-q13.2
381	13
382	1q21.2-22
383	16
384	12
385	20q13.1
386	16
387	8q21.3-q22.1
388	11
389	15q22.1
390	17
391	17
394	8q23
395	15q24-q26
396	15q22
397	7q34-q36
399	2
400	6q21-22
401	6q21-22
402	14q24.3
403	2
404	11q13
405	17
407	14
408	10
409	10q23-q24
410	19
411	11
412	11p15
413	12q13.2-q13.3
414	3p13-q26.1
416	17

SEQ ID	Chromosomal location
421	5q35
422	3
423	12
424	3p24.3
425	19
426	6p21.1-21.2
427	6
428	22q13.2-q13.31
429	11
430	2
432	14q31
433	17
434	22
436	7q35
440	8p11.2
441	11q12
443	5
444	1
445	13q13
446	17
447	17
448	1p35.2-36.13
449	6
450	15q24-q25
451	19
452	4
453	2
454	11
455	17
456	10
457	p31.3-32.2
458	1
459	7p13-p11.2
460	12
461	18p11.2
462	17
463	22q11.2
464	16
466	17
467	11q23
468	3
469	7q32
470	1
472	19
473	19
474	p33-34.3
475	7q36
476	2
477	9p24.1-24.3
478	6p22.1-22.3
479	20
480	22q12.3-13.1
481	16q22.1-q22.3
483	19
484	19
489	6
491	1q21-q22

SEQ ID	Chromosomal location
492	4q26-q27
493	2p13
494	7
495	
496	
497	7q23.2-q25.3
498	11q
499	4p15.31
500	10
501	8q24.3
503	18
504	2
505	19
506	3p14.3
507	14
508	11p15.5
509	11
510	15q25
511	14q21.1-q22.3
512	13q11
513	10
514	Xq28
515	15q15
516	19p13.3
518	14q21
00000385Rd232	
519	13
520	12
521	12
522	20q12-q13.12
523	6q22.1-22.33
524	12
526	16
527	17
528	3
529	6p21.3
530	1q42.13-43
531	16p
532	17
533	16q24.1
534	19p13.3-p13.2
535	19p13.3-p13.2
536	13
537	17
538	12
539	1q21.2-q22
540	17
541	18q12
542	16
545	2p23.3-q34
546	14q21.1-q22.3
547	2p12
548	17q11-qter
549	4
550	17
551	9
552	17q24-q25

SEQ ID	Chromosomal location
553	12
554	5
555	17
556	10q23.3
557	9
558	9
559	x
560	20
562	16
563	15
564	3
565	4
566	6p22.1-23
567	x
568	5
570	19q13.4
572	1p36.23-p36.21
573	6
574	6p11.2-12.3
575	8
577	12
578	17
579	10
580	6p21
581	2
582	3q25.1-q25.2
583	3q25.1-q25.2
584	19
585	19p13.3
586	15
587	15
588	4q25
589	9p24
590	17
591	20q13.11-13.2
592	x
593	2p23.3-q24.3
594	6p22.1
595	1
596	1
597	2q31-q37
598	1p36.1
599	2p11.2-q11.2
600	19p13.1
601	2
602	17p13.3
603	15q
604	11
606	1p36
607	22q11.21
608	3
609	16
610	1
611	6
613	12
615	2p24.3
616	20q11.2

SEQ ID	Chromosomal location
617	16
618	17
619	8q22
620	17q23.1
621	14
622	8
624	17
625	5
626	17
628	19
629	17q11
630	3p21.1-q13.13
631	20
632	20
634	6
636	6
637	2
638	20q13
639	8q22-q23
640	8
642	5q21-q22
643	xq26
644	22
645	11q25
646	2
647	2p23.3-q34
648	5
651	x
652	3
653	3p13-q26.1
654	12q
655	12q
656	17
657	17
658	12
659	12
660	9q31
661	11
663	6
664	2p23.3-q24.3
666	10
667	21q
668	11
669	11
670	21q22.3
671	4p16.1
672	11
673	12
675	19
676	19
677	6p24-25
678	5
679	x
680	3p21.1-q12.3
681	5
683	12p13.1-p12.3
684	17q

SEQ ID	Chromosomal location
685	19
686	19
687	19
688	19
689	7q31.1-q31.3
691	17
692	17
694	X
695	17
697	7p14.3-p14.1
698	5
699	18q12-q21
700	14q24.3
701	17
702	17
703	1
704	20p13
705	6pter-p21.1
706	17
708	8
711	1
712	2p24.3-p24.1
713	16
714	18q21
715	17
716	1q32
717	1q12-21.1
718	18
720	17
721	11
722	11
723	15
724	5
726	7
727	17q21.3
728	11
729	5
730	12
731	4
732	12
733	15q15
734	8q24.3
735	Xq26.3-27.3
736	19q13.2
737	21q22.1
738	5
740	13
742	1p36.2-p35
743	2
744	2
746	1
747	2q32-q33
748	2p23
749	13
750	4
751	17p11.2
752	1p13

SEQ ID	Chromosomal location
753	5
754	11q13.1-q13.3
755	19
756	5pter-p13.3
757	10
758	19q13
760	19
761	14
762	19
763	X
765	X
766	9q34.3
767	17
769	5
770	14
771	17q12
772	20
773	17
774	8
775	3
776	15
777	8
778	6
779	17
780	15
781	14
782	11
783	19q13.4
784	8p11.2
785	8
786	8
787	17
788	8
789	1q42.13-43
790	7q11.21-q11.23
791	11
792	3p13-q13.2
793	9
794	11q12
795	1p32.2-34.2
797	18
798	18
799	11q13
800	17
801	7p15-p21
802	17
803	17p13.1
805	17q25.3
806	17q25
808	5
809	7p15-p14
810	9q34.2-q34.3
811	1
812	6
813	8
814	17
815	20

SEQ ID	Chromosomal location
816	7q34-q36
817	14q21.1-q21.3
818	1p32.1-33
819	5
820	6p21.3
821	17
822	15
823	5
824	19
825	1p32.3
826	11
827	14
828	p34.1-34.3
829	16
830	8p11.2
831	17q21.3-17q22
833	17
834	7p
835	21
836	10cen-q26.11
837	19
838	5
840	10
841	7q11-q22
842	11
843	17
844	3
845	17
846	17
847	17
848	10
849	6
850	5q
851	5
853	7q35-qter
854	19
855	19
857	8
858	16
860	10
861	19
863	18p11.2
864	17
866	15q15
867	7
868	12
869	1
870	11q23
871	16
872	16p13.3
873	17q12-q21
874	11q13.5
875	11cen-q12.1
876	16q13
877	X
878	1q21-q23
879	xq22.1-q22.3

SEQ ID	Chromosomal location
880	1p31.2-32.3
881	19q13.3-q13.4
883	3p
884	7
885	14q32
886	2
887	22q11.2
888	12
889	15
890	18
891	17
892	Xq21.33-22.3
893	6p21.32-22.2
894	11
895	7q33-q34
897	13
898	15
901	1
902	14
904	16p11.2
905	21q22.3
907	10
909	X
910	10q26
911	20
912	1
913	18
914	6
915	10
916	13
917	17
919	15q15
920	20
921	22q12.3
922	16
923	11
924	2q33.3
927	9
928	2q21
929	19
930	18
931	16
932	16
934	11p15
936	7q35
937	6q22.1-22.33
939	17
940	17
941	17
942	4
943	1p36.31-p36.11
944	9
945	12
946	19p13.3
947	22q11.2
948	5

TABLE 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
1	949	1
2	950	2
3	951	3
4	952	4
5	953	5
6	954	6
7	955	7
8	956	8
9	957	9
10	958	10
11	959	11
12	960	12
13	961	13
14	962	14
15	963	15
16	964	16
17	965	17
18	966	18
19	967	19
20	968	20
21	969	21
22	970	22
23	971	23
24	972	24
25	973	25
26	974	26
27	975	27
28	976	28
29	977	29
30	978	30
31	979	31
32	980	32
33	981	33
34	982	34
35	983	35
36	984	36
37	985	37
38	986	38
39	987	39
40	988	40
41	989	41
42	990	42
43	991	43
44	992	44
45	993	45
46	994	46
47	995	47
48	996	48
49	997	49
50	998	50
51	999	51
52	1000	52
53	1001	53
54	1002	54

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
55	1003	55
56	1004	56
57	1005	57
58	1006	58
59	1007	59
60	1008	60
61	1009	61
62	1010	62
63	1011	63
64	1012	64
65	1013	65
66	1014	66
67	1015	67
68	1016	68
69	1017	69
70	1018	70
71	1019	71
72	1020	72
73	1021	73
74	1022	74
75	1023	75
76	1024	76
77	1025	77
78	1026	78
79	1027	79
80	1028	80
81	1029	81
82	1030	82
83	1031	83
84	1032	84
85	1033	85
86	1034	86
87	1035	87
88	1036	88
89	1037	89
90	1038	90
91	1039	91
92	1040	92
93	1041	93
94	1042	94
95	1043	95
96	1044	96
97	1045	97
98	1046	98
99	1047	99
100	1048	100
101	1049	101
102	1050	102
103	1051	103
104	1052	104
105	1053	105
106	1054	106
107	1055	107
108	1056	108
109	1057	109
110	1058	110

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
111	1059	111
112	1060	112
113	1061	113
114	1062	114
115	1063	115
116	1064	116
117	1065	117
118	1066	118
119	1067	119
120	1068	120
121	1069	121
122	1070	122
123	1071	123
124	1072	124
125	1073	125
126	1074	126
127	1075	127
128	1076	128
129	1077	129
130	1078	130
131	1079	131
132	1080	132
133	1081	133
134	1082	134
135	1083	135
136	1084	136
137	1085	137
138	1086	138
139	1087	139
140	1088	140
141	1089	141
142	1090	142
143	1091	143
144	1092	144
145	1093	145
146	1094	146
147	1095	147
148	1096	148
149	1097	149
150	1098	150
151	1099	151
152	1100	152
153	1101	153
154	1102	154
155	1103	155
156	1104	156
157	1105	157
158	1106	158
159	1107	159
160	1108	160
161	1109	161
162	1110	162
163	1111	163
164	1112	164
165	1113	165
166	1114	166

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
167	1115	167
168	1116	168
169	1117	169
170	1118	170
171	1119	171
172	1120	172
173	1121	173
174	1122	174
175	1123	175
176	1124	176
177	1125	177
178	1126	178
179	1127	179
180	1128	180
181	1129	181
182	1130	182
183	1131	183
184	1132	184
185	1133	185
186	1134	186
187	1135	187
188	1136	188
189	1137	189
190	1138	190
191	1139	191
192	1140	192
193	1141	193
194	1142	194
195	1143	195
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204	1152	204
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208	1156	208
209	1157	209
210	1158	210
211	1159	211
212	1160	212
213	1161	213
214	1162	214
215	1163	215
216	1164	216
217	1165	217
218	1166	218
219	1167	219
220	1168	220
221	1169	221
222	1170	222

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
223	1171	223
224	1172	224
225	1173	225
226	1174	226
227	1175	227
228	1176	228
229	1177	229
230	1178	230
231	1179	231
232	1180	232
233	1181	233
234	1182	234
235	1183	235
236	1184	236
237	1185	237
238	1186	238
239	1187	239
240	1188	240
241	1189	241
242	1190	242
243	1191	243
244	1192	244
245	1193	245
246	1194	246
247	1195	247
248	1196	248
249	1197	249
250	1198	250
251	1199	251
252	1200	252
253	1201	253
254	1202	254
255	1203	255
256	1204	256
257	1205	257
258	1206	258
259	1207	259
260	1208	260
261	1209	261
262	1210	262
263	1211	263
264	1212	264
265	1213	265
266	1214	266
267	1215	267
268	1216	268
269	1217	269
270	1218	270
271	1219	271
272	1220	272
273	1221	273
274	1222	274
275	1223	275
276	1224	276
277	1225	277
278	1226	278

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
279	1227	279
280	1228	280
281	1229	281
282	1230	282
283	1231	283
284	1232	284
285	1233	285
286	1234	286
287	1235	287
288	1236	288
289	1237	289
290	1238	290
291	1239	291
292	1240	292
293	1241	293
294	1242	294
295	1243	295
296	1244	296
297	1245	297
298	1246	298
299	1247	299
300	1248	300
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302	1250	302
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305	1253	305
306	1254	306
307	1255	307
308	1256	308
309	1257	309
310	1258	310
311	1259	311
312	1260	312
313	1261	313
314	1262	314
315	1263	315
316	1264	316
317	1265	317
318	1266	318
319	1267	319
320	1268	320
321	1269	321
322	1270	322
323	1271	323
324	1272	324
325	1273	325
326	1274	326
327	1275	327
328	1276	328
329	1277	329
330	1278	330
331	1279	331
332	1280	332
333	1281	333
334	1282	334

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
335	1283	335
336	1284	336
337	1285	337
338	1286	338
339	1287	339
340	1288	340
341	1289	341
342	1290	342
343	1291	343
344	1292	344
345	1293	345
346	1294	346
347	1295	347
348	1296	348
349	1297	349
350	1298	350
351	1299	351
352	1300	352
353	1301	353
354	1302	354
355	1303	355
356	1304	356
357	1305	357
358	1306	358
359	1307	359
360	1308	360
361	1309	361
362	1310	362
363	1311	363
364	1312	364
365	1313	365
366	1314	366
367	1315	367
368	1316	368
369	1317	369
370	1318	370
371	1319	371
372	1320	372
373	1321	373
374	1322	374
375	1323	375
376	1324	376
377	1325	377
378	1326	378
379	1327	379
380	1328	380
381	1329	381
382	1330	382
383	1331	383
384	1332	384
385	1333	385
386	1334	386
387	1335	387
388	1336	388
389	1337	389
390	1338	390

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
391	1339	391
392	1340	392
393	1341	393
394	1342	394
395	1343	395
396	1344	396
397	1345	397
398	1346	398
399	1347	399
400	1348	400
401	1349	401
402	1350	402
403	1351	403
404	1352	404
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418	1366	418
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420	1368	420
421	1369	421
422	1370	422
423	1371	423
424	1372	424
425	1373	425
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428	1376	428
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430	1378	430
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432	1380	432
433	1381	433
434	1382	434
435	1383	435
436	1384	436
437	1385	437
438	1386	438
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445	1393	445
446	1394	446

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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500	1448	500
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502	1450	502

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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620	1568	620
621	1569	621
622	1570	622
623	1571	623
624	1572	624
625	1573	625
626	1574	626
627	1575	627
628	1576	628
629	1577	629
630	1578	630
631	1579	631
632	1580	632
633	1581	633
634	1582	634
635	1583	635
636	1584	636
637	1585	637
638	1586	638
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642	1590	642
643	1591	643
644	1592	644
645	1593	645
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660	1608	660
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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714	1662	714
715	1663	715
716	1664	716
717	1665	717
718	1666	718
719	1667	719
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721	1669	721
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723	1671	723
724	1672	724
725	1673	725
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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729	1677	729
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732	1680	732
733	1681	733
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747	1695	747
748	1696	748
749	1697	749
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768	1716	768
769	1717	769
770	1718	770
771	1719	771
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780	1728	780
781	1729	781
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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789	1737	789
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792	1740	792
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810	1758	810
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812	1760	812
813	1761	813
814	1762	814
815	1763	815
816	1764	816
817	1765	817
818	1766	818
819	1767	819
820	1768	820
821	1769	821
822	1770	822
823	1771	823
824	1772	824
825	1773	825
826	1774	826
827	1775	827
828	1776	828
829	1777	829
830	1778	830
831	1779	831
832	1780	832
833	1781	833
834	1782	834
835	1783	835
836	1784	836
837	1785	837
838	1786	838

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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843	1791	843
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845	1793	845
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847	1795	847
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849	1797	849
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852	1800	852
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863	1811	863
864	1812	864
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866	1814	866
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870	1818	870
871	1819	871
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878	1826	878
879	1827	879
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882	1830	882
883	1831	883
884	1832	884
885	1833	885
886	1834	886
887	1835	887
888	1836	888
889	1837	889
890	1838	890
891	1839	891
892	1840	892
893	1841	893
894	1842	894

<u>SEQ ID NO of Full-length Nucleotide Sequence</u>	<u>SEQ ID NO of Full-length Peptide Sequence</u>	<u>SEQ ID NO in Priority Application USSN 09/799,451</u>
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896	1844	896
897	1845	897
898	1846	898
899	1847	899
900	1848	900
901	1849	901
902	1850	902
903	1851	903
904	1852	904
905	1853	905
906	1854	906
907	1855	907
908	1856	908
909	1857	909
910	1858	910
911	1859	911
912	1860	912
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914	1862	914
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917	1865	917
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919	1867	919
920	1868	920
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922	1870	922
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927	1875	927
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929	1877	929
930	1878	930
931	1879	931
932	1880	932
933	1881	933
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937	1885	937
938	1886	938
939	1887	939
940	1888	940
941	1889	941
942	1890	942
943	1891	943
944	1892	944
945	1893	945
946	1894	946
947	1895	947
948	1896	948

CLAIMS**WHAT IS CLAIMED IS:**

- 5 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 948, a mature protein coding portion of SEQ ID NO: 1 – 948, an active domain coding protein of SEQ ID NO: 1 – 948, and complementary sequences thereof.
- 10 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 15 3. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
4. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 20 5. A vector comprising the polynucleotide of claim 1.
6. An expression vector comprising the polynucleotide of claim 1.
- 25 7. A host cell genetically engineered to comprise the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 30 9. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of a polypeptide encoded by any one of the polynucleotides of claim 1 (i.e. SEQ ID NO: 949-1896).
10. A composition comprising the polypeptide of claim 9 and a carrier.

11. An antibody directed against the polypeptide of claim 9.

12. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- 5 a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- 10 a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

 b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
15 c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

20 14. The method of claim 13, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

15. A method for detecting the polypeptide of claim 9 in a sample, comprising:

- 25 a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 9 is detected.

30 16. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

- a) contacting the compound with the polypeptide of claim 9 under conditions sufficient to form a polypeptide/compound complex; and
 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

17. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

5 a) contacting the compound with the polypeptide of claim 9, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

10 b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

15 18. A method of producing the polypeptide of claim 9, comprising,

18 a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-948, a mature protein coding portion of SEQ ID NO: 1-948, an active domain coding portion of SEQ ID NO: 1-948, complementary sequences thereof, under conditions sufficient to express the polypeptide in said cell; and

20 b) isolating the polypeptide from the cell culture or cells of step (a).

25 19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

20 20. The polypeptide of claim 21 wherein the polypeptide is provided on a polypeptide array.

25 21. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 948.

30 22. The collection of claim 21, wherein the collection is provided on a nucleic acid array.

23. The collection of claim 22, wherein the array detects full-matches to any one of the polynucleotides in the collection.

24. The collection of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection.

5 25. The collection of claim 21, wherein the collection is provided in a computer-readable format.

26. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.

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27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.